

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 18:28:36 : Search time 35 Seconds
(without alignments)
102.793 Million cell updates/sec

Title: US-09-666-837B-1

Perfect score: 120
Sequence: 1 CXIXNQXCKQXLDCCSXXCNXXNXCXV 27

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapept 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: A_Geneseq_101002:.*
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21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	100.0	27	18 AAW35723	Kappa-conotoxin PV
2	120	100.0	27	22 AAU10195	Snail Kappa-conoto
3	120	100.0	27	22 AAU10196	Snail Kappa-conoto
4	120	100.0	27	22 AAU10197	Snail Kappa-conoto
5	120	100.0	27	22 AAU10199	Snail Kappa-conoto
6	120	100.0	27	22 AAU10200	Snail Kappa-conoto
7	120	100.0	27	22 AAU10201	Snail Kappa-conoto
8	120	100.0	27	22 AAU10202	Snail Kappa-conoto
9	120	100.0	27	22 AAU10203	Snail Kappa-conoto
10	120	100.0	27	22 AAU10204	Snail Kappa-conoto

11	120	100.0	27	22 AAU10205	Snail Kappa-conoto
12	120	100.0	27	22 AAU10206	Snail Kappa-conoto
13	120	100.0	27	22 AAU10207	Snail Kappa-conoto
14	120	100.0	27	22 AAU10208	Snail Kappa-conoto
15	120	100.0	27	22 AAU10218	Snail Kappa-conoto
16	117	97.5	27	22 AAU10212	Snail Kappa-conoto
17	116	96.7	27	22 AAU10217	Snail Kappa-conoto
18	115	95.8	27	22 AAU10198	Snail Kappa-conoto
19	115	95.8	27	22 AAU10214	Snail Kappa-conoto
20	114	95.0	27	22 AAU10210	Snail Kappa-conoto
21	114	95.0	27	22 AAU10216	Snail Kappa-conoto
22	112	93.3	27	22 AAU10209	Snail Kappa-conoto
23	112	93.3	27	22 AAU10211	Snail Kappa-conoto
24	112	93.3	27	22 AAU10213	Snail Kappa-conoto
25	112	93.3	27	22 AAU10215	Snail Kappa-conoto
26	112	93.3	27	22 AAU10219	Snail Kappa-conoto
27	81	67.5	26	14 AAR37774	SNX-202. Syntheti
28	81	67.5	26	14 AAR39628	SNX-202. Syntheti
29	81	67.5	26	18 AAW19570	SNX-202, omega con
30	81	67.5	26	18 AAW12985	Omega conopeptide
31	81	67.5	26	19 AAW72625	Conus genus analog
32	81	67.5	26	20 AAW95584	Analog omega-conop
33	81	67.5	26	21 AAB14370	Omega-conopeptide
34	81	67.5	26	21 AAY56496	Analog omega con
35	81	67.5	26	22 AAB19462	Sequence of an ome
36	81	67.5	26	23 ABB96887	Omega-conopeptide
37	81	67.5	30	23 ABB96679	Omega-conopeptide
38	77	64.2	26	14 AAR37760	SVIB/SNX-183. Syn
39	77	64.2	26	14 AAR39615	SVIB/SNX183. Syn
40	77	64.2	26	18 AAW19551	Natural omega-cono
41	77	64.2	26	18 AAW12974	Omega conopeptide
42	77	64.2	26	18 AAW72612	Conus genus natura
43	77	64.2	26	20 AAW95571	Omega-conopeptide
44	77	64.2	26	21 AAB14359	Omega-conopeptide
45	77	64.2	26	21 AAY56480	Natural omega cono

ALIGNMENTS

RESULT 1	
ID AAW35723	standard; peptide; 27 AA.
XX AAW35723:	
XX 03-APR-1998 (first entry)	
XX	Kappa-conotoxin PV1A.
DE	Kappa-conotoxin PV1A.
XX	Kappa-conotoxin PV1A; potassium channel; neurotransmitter release;
KW	cone snail; venom; goldfish; delta-conotoxin PV1A; disulphide.
XX	
OS	Conus purpurascens.
XX	
PH	Key
FT	Modified-site
FT	Location/Qualifiers
FT	/note= "Optionally 4-trans-hydroxyproline, hydroxyproline or proline"
FT	Disulfide-bond 1..16
FT	/note= "disulphide bond"
FT	Disulfide-bond 8..20
FT	/note= "disulphide bond"
FT	Disulfide-bond 15..26
FT	/note= "disulphide bond"
PN	WO9734925-A1.
XX	
PD	25-SEP-1997.
XX	
XX	14-MAR-1997; 97WO-US03483.
PF	
XX	
PR	18-MAR-1996; 96US-0619936.

XX	PA	(UTAH) UNIV UTAH RES FOUND.
XX	PI	Grilley MM, Olivera BM, Shon K, Terlau H;
XX	DR	WPI; 1997-480162/44.
XX	PT	New kappa-conotoxin peptides - which target potassium channels and
XX	PT	can be used to augment neurotransmitter release in e.g. autoimmune
XX	PT	diseases.
PS	XX	Claim 1; Page 23; 29pp; English.
CC	CC	The present sequence represents a new kappa-conotoxin PVIIA which
CC	CC	targets potassium channels and can be used to augment neurotransmitter
CC	CC	release in pathological situations such as autoimmune diseases, e.g. '
CC	CC	Alzheimer's disease, Lambert-Paton syndrome or myasthenia gravis.
CC	CC	This peptide together with delta-conotoxin PVIIA act synergistically to
CC	CC	rapidly immobilize fish which are injected with the two peptides.
CC	CC	Injection of kappa-conotoxin PVIIA alone results in different symptoms
CC	CC	with an injected fish becoming hyperactive and then contracting and
CC	CC	suddenly extending all major fins. This "fin-popping" occurs repeatedly
CC	CC	resulting in a series of jerky movements, but injection of only
CC	CC	kappa-conotoxin PVIIA does not immobilize or kill the fish.
SO	Sequence	27 AA;
QY	Query Match	100.0%; Score 120; DR 18; Length 27;
DB	Best Local Similarity	63.0%; Pred. No. 0.00036;
DB	Matches 17; Conservative 10; Mismatches 0;	Indels 0; Gaps 0;
QY	1	CXIXNQXQXQXLDGCCXXCXNXXNXCXV 27
DB	1	CRIPNCKCFQHLDDCCSRKCNRFNKCXV 27
QY	1	: : : : :
DB	1	: : : : :
RESULT 2		
ID	AAU010195	standard; peptide; 27 AA.
XX	AAU010195;	
XX	16-JAN-2002 (first entry)	
DE	Small Kappa-conotoxin PVIIA analogue #1.	
XX	Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;	
KW	cardioactive; antilasthmatic; KATP channel activation; cardiac ischaemia;	
KW	cerebral ischaemia; ocular ischaemia; asthma.	
XX	Conus purpurascens.	
OS	Synthetic.	
XX		
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 2	/label- OTHER
FT		/note= "Other- Arg, homoaArg, ornithine, Lys,
FT		N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys,
FT		any synthetic basic amino acid, His or halo-His"
FT	Misc-difference 4	/label- OTHER
FT		/note= "Other- Pro or Hydroxyproline"
FT	Misc-difference 7	/label- OTHER
FT		/note= "Other- Arg, homoaArg, ornithine, Lys,
FT		N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys,
FT		any synthetic basic amino acid, His or halo-His"
FT	Misc-difference 9	/label- OTHER
FT		/note= "Other- Phe, Tyr, meta-Tyr, ortho-Tyr,
FT		nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
FT		O-phospho-Tyr, nitro-Tyr, (D,L)-Tyr, neo-Tyr or
FT		(D,L)-halo-Tyr"

Seq	Accession	Protein	Score	DB	Length	Mismatches	Indels	Gaps
1	U00001	11	100.0%	DB 22:	27	0	0	0
2	U00001	18	100.0%	DB 22:	27	0	0	0
3	U00001	19	100.0%	DB 22:	27	0	0	0
4	U00001	20	100.0%	DB 22:	27	0	0	0
5	U00001	21	100.0%	DB 22:	27	0	0	0
6	U00001	22	100.0%	DB 22:	27	0	0	0
7	U00001	23	100.0%	DB 22:	27	0	0	0
8	U00001	24	100.0%	DB 22:	27	0	0	0
9	U00001	25	100.0%	DB 22:	27	0	0	0
10	U00001	26	100.0%	DB 22:	27	0	0	0
11	U00001	27	100.0%	DB 22:	27	0	0	0
12	U00001	28	100.0%	DB 22:	27	0	0	0
13	U00001	29	100.0%	DB 22:	27	0	0	0
14	U00001	30	100.0%	DB 22:	27	0	0	0
15	U00001	31	100.0%	DB 22:	27	0	0	0
16	U00001	32	100.0%	DB 22:	27	0	0	0
17	U00001	33	100.0%	DB 22:	27	0	0	0
18	U00001	34	100.0%	DB 22:	27	0	0	0
19	U00001	35	100.0%	DB 22:	27	0	0	0
20	U00001	36	100.0%	DB 22:	27	0	0	0
21	U00001	37	100.0%	DB 22:	27	0	0	0
22	U00001	38	100.0%	DB 22:	27	0	0	0
23	U00001	39	100.0%	DB 22:	27	0	0	0
24	U00001	40	100.0%	DB 22:	27	0	0	0
25	U00001	41	100.0%	DB 22:	27	0	0	0
26	U00001	42	100.0%	DB 22:	27	0	0	0
27	U00001	43	100.0%	DB 22:	27	0	0	0
28	U00001	44	100.0%	DB 22:	27	0	0	0
29	U00001	45	100.0%	DB 22:	27	0	0	0
30	U00001	46	100.0%	DB 22:	27	0	0	0
31	U00001	47	100.0%	DB 22:	27	0	0	0
32	U00001	48	100.0%	DB 22:	27	0	0	0
33	U00001	49	100.0%	DB 22:	27	0	0	0
34	U00001	50	100.0%	DB 22:	27	0	0	0
35	U00001	51	100.0%	DB 22:	27	0	0	0
36	U00001	52	100.0%	DB 22:	27	0	0	0
37	U00001	53	100.0%	DB 22:	27	0	0	0
38	U00001	54	100.0%	DB 22:	27	0	0	0
39	U00001	55	100.0%	DB 22:	27	0	0	0
40	U00001	56	100.0%	DB 22:	27	0	0	0
41	U00001	57	100.0%	DB 22:	27	0	0	0
42	U00001	58	100.0%	DB 22:	27	0	0	0
43	U00001	59	100.0%	DB 22:	27	0	0	0
44	U00001	60	100.0%	DB 22:	27	0	0	0
45	U00001	61	100.0%	DB 22:	27	0	0	0
46	U00001	62	100.0%	DB 22:	27	0	0	0
47	U00001	63	100.0%	DB 22:	27	0	0	0
48	U00001	64	100.0%	DB 22:	27	0	0	0
49	U00001	65	100.0%	DB 22:	27	0	0	0
50	U00001	66	100.0%	DB 22:	27	0	0	0
51	U00001	67	100.0%	DB 22:	27	0	0	0
52	U00001	68	100.0%	DB 22:	27	0	0	0
53	U00001	69	100.0%	DB 22:	27	0	0	0
54	U00001	70	100.0%	DB 22:	2			

Db 1 CXTXNKCXQXLDCCSXKCNXKCV 27

RESULT 3
AAU10196
ID AAU10196 standard; peptide: 27 AA.

AC AAU10196;

DT 16-JAN-2002 (first entry)

DE Snail Kappa-conotoxin PVIIA analogue R18A.

KM Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; R18A.

OS Conus purpurascens.
XX Synthetic.

FT Key Location/Qualifiers
FT Modified-site 4

FT Modified-site /note= "Hydroxyproline"

FT /note= "The C-terminus is either a carboxyl group
or an amide group"

PN W0200121648-A1.

PD 29-MAR-2001.

PF 21-SEP-2000; 2000MO-US25827.

PR 22-SEP-1999; 99US-155135P.

PR 20-JUL-2000; 2000US-0219438.

PA (COGN-) COGNETIX INC.

PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;

PI Jones RR;

PT WPI; 2001-648090/74.

PS Claim 1; Page 27; 46pp; English.

CC The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA
CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
CC active salt. The conotoxins are used for treating disorders associated
CC with radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin
CC PVIIA analogue of the invention.

SO Sequence 27 AA;

Query Match 100.0%; Score 120; DB 22; Length 27;
Best Local Similarity 66.7%; Pred. No. 0.00036;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXTXNKCXQXLDCCSXKCNXKCV 27
ID 1 CXTXNKCXQXLDCCSXKCNXKCV 27

RESULT 4

AAU10197
ID AAU10197 standard; peptide: 27 AA.

AC AAU10197;

DT 16-JAN-2002 (first entry)

DE Snail Kappa-conotoxin PVIIA analogue R22A.

KM Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; R22A.

OS Conus purpurascens.
XX Synthetic.

FT Key Location/Qualifiers
FT Modified-site 4

FT Modified-site /note= "Hydroxyproline"

FT /note= "The C-terminus is either a carboxyl group
or an amide group"

PN W0200121648-A1.

PD 29-MAR-2001.

PF 21-SEP-2000; 2000MO-US25827.

PR 22-SEP-1999; 99US-155135P.

PR 20-JUL-2000; 2000US-0219438.

PA (COGN-) COGNETIX INC.

PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;

PI Jones RR;

PT WPI; 2001-648090/74.

PS Claim 1; Page 27; 46pp; English.

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CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA
CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
CC active salt. The conotoxins are used for treating disorders associated
CC with radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin
CC PVIIA analogue of the invention.

SO Sequence 27 AA;

Query Match 100.0%; Score 120; DB 22; Length 27;
Best Local Similarity 66.7%; Pred. No. 0.00036;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXTXNKCXQXLDCCSXKCNXKCV 27
ID 1 CXTXNKCXQXLDCCSXKCNXKCV 27

RESULT 5
AAU10199
ID AAU10199 standard; peptide: 27 AA.

AC AAU10199;

DT 16-JAN-2002 (first entry)
XX Snail Kappa-conotoxin PVIIA analogue K19A.
DE Purple cone snail; Kappa-conotoxin PVIIA analogue; circulatory;
XX cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; K19A.
XX
OS Conus purpurascens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 4
FT /note= "Hydroxyproline"
FT Modified-site 27
FT /note= "The C-terminus is either a carboxyl group
FT or an amide group"
XX
XX WO200121648-A1.
XX
XX 29-MAR-2001.
XX
XX 21-SEP-2000; 2000WO-US25827.
XX
XX 22-SEP-1999; 99US-155135P.
XX 20-JUL-2000; 2000US-0219438.
XX
XX (COGN-) COGNETIX INC.
XX
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
XX Jones RR;
XX
XX WPI; 2001-648090/74.
XX
XX Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma
PT comprises activating a KATP channel by administering to an individual a
PT kappa-conotoxin PVIIA peptide -
XX
XX Claim 1; Page 27; 46pp; English.
XX
XX The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA
CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
CC active salt. The conotoxins are used for treating disorders associated
CC with radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin
CC PVIIA analogue of the invention.
XX
SQ Sequence 27 AA:

Query Match 100.0%; Score 120; DB 22; Length 27;
Best Local Similarity 66.7%; Pred. No. 0.00036;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXTXNQXCXQXLDCCSXKXNKNXCV 27
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Db 1 CXTXNQXCXQXLDCCSXKXNKNXCV 27

RESULT 6
AAU10200
ID AAU10200 standard; peptide: 27 AA.
XX
AC AAU10200;
XX
DT 16-JAN-2002 (first entry)
XX
XX Snail Kappa-conotoxin PVIIA analogue R2A.
DE
XX Purple cone snail; Kappa-conotoxin PVIIA analogue; circulatory;
KW cerebral ischaemia; ocular ischaemia; asthma; K19A.
XX
OS Conus purpurascens.
OS Synthetic.

KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; R2A.
XX
OS Conus purpurascens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 4
FT /note= "Hydroxyproline"
FT Modified-site 27
FT /note= "The C-terminus is either a carboxyl group
FT or an amide group"
XX
XX WO200121648-A1.
XX
XX 29-MAR-2001.
XX
XX 21-SEP-2000; 2000WO-US25827.
XX
XX 22-SEP-1999; 99US-155135P.
XX 20-JUL-2000; 2000US-0219438.
XX
XX (COGN-) COGNETIX INC.
XX
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
XX Jones RR;
XX
XX WPI; 2001-648090/74.
XX
XX Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma
PT comprises activating a KATP channel by administering to an individual a
PT kappa-conotoxin PVIIA peptide -
XX
XX Claim 1; Page 27; 46pp; English.
XX
XX The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA
CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
CC active salt. The conotoxins are used for treating disorders associated
CC with radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin
CC PVIIA analogue of the invention.
XX
SQ Sequence 27 AA:

Query Match 100.0%; Score 120; DB 22; Length 27;
Best Local Similarity 66.7%; Pred. No. 0.00036;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXTXNQXCXQXLDCCSXKXNKNXCV 27
1:|||||:|:|||||:|:|||||:|:|||||
Db 1 CXTXNQXCXQXLDCCSXKXNKNXCV 27

RESULT 7
AAU10201
ID AAU10201 standard; peptide: 27 AA.
XX
AC AAU10201;
XX
DT 16-JAN-2002 (first entry)
XX
XX Snail Kappa-conotoxin PVIIA analogue F9A.
DE
XX Purple cone snail; Kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; F9A.
XX
OS Conus purpurascens.
OS Synthetic.

XX Key Location/Qualifiers
 FT Modified-site 4 /note="Hydroxyproline"
 FT Modified-site 27 /note="The C-terminus is either a carboxyl group
 or an amide group"
 FT
 XX WO200121648-A1.
 PN 29-MAR-2001.
 PD 21-SEP-2000; 2000WO-US25827.
 XX 22-SEP-1999; 99US-155135P.
 PR 20-JUL-2000; 2000US-0219438.
 XX
 XX (COGN-) COGNETIX INC.
 PA Corneli-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 XX WPI; 2001-648090/74.
 DR
 XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma
 PT comprises activating a KATP channel by administering to an individual a
 PT kappa-conotoxin PVIIA peptide -
 XX
 PS Claim 1; Page 27; 46pp; English.
 XX
 CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA
 CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
 CC active salt. The conotoxins are used for treating disorders associated
 CC with radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin
 CC PVIIA analogue of the invention.
 CC
 XX
 SO Sequence 27 AA;
 QY
 Query Match 100.0%; Score 120; DB 22; Length 27;
 Best Local Similarity 66.7%; Pred. No. 0.00036;
 Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
 DB 1 CRXNOKCXOHLDCCSRKXNKNXCV 27
 1 CRXNOKCXOHLDCCSRKXNKNXCV 27
 RESULT 8
 AAU10202
 ID AAU10202 standard; peptide; 27 AA.
 XX
 AC AAU10202;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE Snail Kappa-conotoxin PVIIA analogue K25A.
 XX
 KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiaesthetic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; K25A.
 XX
 OS Conus purpurascens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 4 /note="Hydroxyproline"
 FT Modified-site 27 /note="The C-terminus is either a carboxyl group
 or an amide group"

FT /note="The C-terminus is either a carboxyl group
 or an amide group"
 FT
 XX WO200121648-A1.
 PN 29-MAR-2001.
 PD 21-SEP-2000; 2000WO-US25827.
 XX 22-SEP-1999; 99US-155135P.
 PR 20-JUL-2000; 2000US-0219438.
 XX
 XX (COGN-) COGNETIX INC.
 PA Corneli-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 XX WPI; 2001-648090/74.
 DR
 XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma
 PT comprises activating a KATP channel by administering to an individual a
 PT kappa-conotoxin PVIIA peptide -
 XX
 PS Claim 1; Page 27; 46pp; English.
 XX
 CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA
 CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
 CC active salt. The conotoxins are used for treating disorders associated
 CC with radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin
 CC PVIIA analogue of the invention.
 CC
 XX
 SO Sequence 27 AA;
 QY
 Query Match 100.0%; Score 120; DB 22; Length 27;
 Best Local Similarity 66.7%; Pred. No. 0.00036;
 Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
 DB 1 CRXNOKCFOHLDCCSRKXNKNXCV 27
 1 CRXNOKCFOHLDCCSRKXNKNXCV 27
 RESULT 9
 AAU10203
 ID AAU10203 standard; peptide; 27 AA.
 XX
 AC AAU10203;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE Snail Kappa-conotoxin PVIIA analogue R2K.
 XX
 KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiaesthetic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; R2K.
 XX
 OS Conus purpurascens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 4 /note="Hydroxyproline"
 FT Modified-site 27 /note="The C-terminus is either a carboxyl group
 or an amide group"
 FT
 XX WO200121648-A1.

PD 29-MAR-2001.
XX
XX 21-SEP-2000; 2000MO-US25827.
XX
XX 22-SEP-1999; 99US-155135P.
PR 20-JUL-2000; 2000US-0219438.
XX
XX (COGN-) COGNETIX INC.
XX
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
DR WPI: 2001-648090/74.
XX
XX Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma
PT comprises activating a KATP channel by administering to an individual a
PT kappa-conotoxin PVIIA peptide -
XX
XX Claim 1; Page 27; 46pp; English.
XX
XX The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA
CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
CC active salt. The conotoxins are used for treating disorders associated
CC with radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischemia, cerebral ischemia, ocular
CC ischemia and asthma. The present sequence is a kappa-conotoxin
CC PVIIA analogue of the invention.
XX
XX Sequence 27 AA;
SQ
Query Match 100.0%; Score 120; DB 22; Length 27;
Best Local Similarity 66.7%; Pred. No. 0.00036;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
OY 1 CXINQXQXLDCCSXKXNXCXV 27
DB 1 CXINQXCFQHLDDCCSRKCNRFKCV 27
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AAU10204
ID AAU10204 standard; peptide: 27 AA.
XX
XX AAU10204;
AC
XX 16-JAN-2002 (first entry)
DT
XX
XX Snail Kappa-conotoxin PVIIA analogue K7A.
DE
XX
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antihistaminic; KATP channel activation; cardiac ischemia;
KW cerebral ischemia; ocular ischemia; asthma; K7A.
XX
XX Conus purpurascens.
OS Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 4 /note= "Hydroxyproline"
FT
FT Modified-site 27 /note= "The C-terminus is either a carboxyl group
FT or an amide group"
FT
XX
XX WO200121648-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 21-SEP-2000; 2000MO-US25827.
PR
XX
XX 22-SEP-1999; 99US-155135P.
PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;

PR 20-JUL-2000; 2000US-0219438.
XX
XX (COGN-) COGNETIX INC.
XX
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
DR WPI: 2001-648090/74.
XX
XX Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma
PT comprises activating a KATP channel by administering to an individual a
PT kappa-conotoxin PVIIA peptide -
XX
XX Claim 1; Page 28; 46pp; English.
XX
XX The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA
CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
CC active salt. The conotoxins are used for treating disorders associated
CC with radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischemia, cerebral ischemia, ocular
CC ischemia and asthma. The present sequence is a kappa-conotoxin
CC PVIIA analogue of the invention.
XX
XX Sequence 27 AA;
SQ
Query Match 100.0%; Score 120; DB 22; Length 27;
Best Local Similarity 66.7%; Pred. No. 0.00036;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
OY 1 CXINQXQXLDCCSXKXNXCXV 27
DB 1 CXINQXCFQHLDDCCSRKCNRFKCV 27
1
RESULT 11
AAU10205
ID AAU10205 standard; peptide: 27 AA.
XX
XX AAU10205;
AC
XX 16-JAN-2002 (first entry)
DT
XX
XX Snail Kappa-conotoxin PVIIA analogue P9M.
DE
XX
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antihistaminic; KATP channel activation; cardiac ischemia;
KW cerebral ischemia; ocular ischemia; asthma; P9M.
XX
XX Conus purpurascens.
OS Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 4 /note= "Hydroxyproline"
FT
FT Modified-site 27 /note= "The C-terminus is either a carboxyl group
FT or an amide group"
FT
XX
XX WO200121648-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 21-SEP-2000; 2000MO-US25827.
PR
XX
XX 22-SEP-1999; 99US-155135P.
PR 20-JUL-2000; 2000US-0219438.
XX
XX (COGN-) COGNETIX INC.
XX
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;

PI Jones RR;
 XX WPI: 2001-648090/74.
 DR
 XX
 PT Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma
 PT comprises activating a KATP channel by administering to an individual a
 PT kappa-conotoxin PVIIA peptide -
 XX
 PS Claim 1; Page 28; 46pp; English.
 CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA
 CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
 CC active salt. The conotoxins are used for treating disorders associated
 CC with radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin
 CC PVIIA analogue of the invention.
 CC
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 120; DB 22; Length 27;
 Best Local Similarity 66.7%; Pred. No. 0.00036;
 Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXIXNQCKQXLDCCSXKCNKXNCV 27
 1:|||||:|:|||||:|:|:|:|
 DB 1 CRXNQCKQXLDCCSRKCNRFKCV 27
 1:|||||:|:|||||:|:|:|:|
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 AAU10206
 ID AAU10206 standard; peptide; 27 AA.
 AC AAU10206;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE Small Kappa-conotoxin PVIIA analogue F9Y.
 XX
 KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; F9Y.
 XX
 OS Conus purpurascens.
 OS Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4 /note= "Hydroxyproline"
 FT Modified-site 27 /note= "The C-terminus is either a carboxyl group
 FT or an amide group"
 XX
 PN WO200121648-A1.
 PD 29-MAR-2001.
 PF 21-SEP-2000; 2000WO-US25827.
 XX
 PR 22-SEP-1999; 99US-155135P.
 PR 20-JUL-2000; 2000US-0219438.
 XX
 PA (COGN-) COGNETIX INC.
 XX
 PI Cornelli-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 XX WPI: 2001-648090/74.
 DR
 XX
 PT Treating disorders associated with radical depolarization of excitable

PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma
 PT comprises activating a KATP channel by administering to an individual a
 PT kappa-conotoxin PVIIA peptide -
 XX
 PS Claim 1; Page 28; 46pp; English.
 CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA
 CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
 CC active salt. The conotoxins are used for treating disorders associated
 CC with radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin
 CC PVIIA analogue of the invention.
 CC
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 120; DB 22; Length 27;
 Best Local Similarity 66.7%; Pred. No. 0.00036;
 Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXIXNQCKQXLDCCSXKCNKXNCV 27
 1:|||||:|:|||||:|:|:|:|
 DB 1 CRXNQCKQXLDCCSRKCNRFKCV 27
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 RESULT 13
 AAU10207
 ID AAU10207 standard; peptide; 27 AA.
 AC AAU10207;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE Small Kappa-conotoxin PVIIA analogue R2Q.
 XX
 KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; R2Q.
 XX
 OS Conus purpurascens.
 OS Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4 /note= "Hydroxyproline"
 FT Modified-site 27 /note= "The C-terminus is either a carboxyl group
 FT or an amide group"
 XX
 PN WO200121648-A1.
 PD 29-MAR-2001.
 PF 21-SEP-2000; 2000WO-US25827.
 XX
 PR 22-SEP-1999; 99US-155135P.
 PR 20-JUL-2000; 2000US-0219438.
 XX
 PA (COGN-) COGNETIX INC.
 XX
 PI Cornelli-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 XX WPI: 2001-648090/74.
 DR
 XX
 PT Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma
 PT comprises activating a KATP channel by administering to an individual a
 PT kappa-conotoxin PVIIA peptide -
 XX
 PS Claim 1; Page 28; 46pp; English.

XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KARP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA
 CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
 CC active salt. The conotoxins are used for treating disorders associated
 CC with radical depolarisation of excitable membrane by activating a KARP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin
 CC PVIIA analogue of the invention.
 XX
 SQ Sequence 27 AA:

Query Match 100.0%; Score 120; DB 22; Length 27;
 Best Local Similarity 66.7%; Pred. No. 0.00036;
 Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXINQXCXQXLDCCSXKCNXXKCV 27
 DB 1 COIXNKCFOHLDCCSRKCNFKVCV 27

RESULT 14

AAU10208 standard; peptide: 27 AA.

AC AAU10208;

DT 16-JAN-2002 (first entry)

DE Small Kappa-conotoxin PVIIA analogue H1A.

XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;

KW cardioactive; antisthmatic; KARP channel activation; cardiac ischaemia;

KW cerebral ischaemia; ocular ischaemia; asthma; H1A.

XX Conus purpurascens.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 4 /note= "Hydroxyproline"

FT Modified-site 27 /note= "The C-terminus is either a carboxyl group

FT or an amide group"

XX WO200121648-A1.

XX 29-MAR-2001.

PF 21-SEP-2000; 2000WO-US25827.

XX 22-SEP-1999; 99US-155135P.

PR 20-JUL-2000; 2000US-0219438.

XX (COGN-) COGNETIX INC.

XX Corneli-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;

PI Jones RR;

XX WPI; 2001-648090/74.

XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma
 PT comprises administering to an individual a kappa-conotoxin PVIIA peptide -

XX Claim 1; Page 28; 46pp; English.

XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KARP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA
 CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically

CC active salt. The conotoxins are used for treating disorders associated
 CC with radical depolarisation of excitable membrane by activating a KARP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin
 CC PVIIA analogue of the invention.
 XX
 SQ Sequence 27 AA:

Query Match 100.0%; Score 120; DB 22; Length 27;
 Best Local Similarity 66.7%; Pred. No. 0.00036;
 Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXINQXCXQXLDCCSXKCNXXKCV 27
 DB 1 COIXNKCFOHLDCCSRKCNFKVCV 27

RESULT 15

AAU10218 standard; peptide: 27 AA.

AC AAU10218;

DT 16-JAN-2002 (first entry)

DE Small Kappa-conotoxin PVIIA analogue O4A.

XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;

KW cardioactive; antisthmatic; KARP channel activation; cardiac ischaemia;

KW cerebral ischaemia; ocular ischaemia; asthma; O4A.

XX Conus purpurascens.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 4 /note= "Hydroxyproline"

FT Modified-site 27 /note= "The C-terminus is either a carboxyl group

FT or an amide group"

XX WO200121648-A1.

XX 29-MAR-2001.

PF 21-SEP-2000; 2000WO-US25827.

XX 22-SEP-1999; 99US-155135P.

PR 20-JUL-2000; 2000US-0219438.

XX (COGN-) COGNETIX INC.

XX Corneli-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;

PI Jones RR;

XX WPI; 2001-648090/74.

XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma
 PT comprises administering to an individual a kappa-conotoxin PVIIA peptide -

XX Claim 1; Page 28; 46pp; English.

XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KARP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA
 CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
 CC active salt. The conotoxins are used for treating disorders associated
 CC with radical depolarisation of excitable membrane by activating a KARP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin
 CC PVIIA analogue of the invention.

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Query Match	100.0%;	Score 120;	DB 22;	Length 27;
Best Local Similarity	63.0%;	Pred. No. 0.00036;		
Matches 17; Conservative	10;	Mismatches 0;	Indels 0;	Gaps 0;

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Job time : 36 secs

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OM protein - protein search, using sw model

Run on: January 14, 2003, 18:30:11 ; Search time 14 Seconds
(without alignments)

56,744 Million cell updates/sec

Title: US-09-666-837B-1

Perfect score: 120

Sequence: 1 CXIXNQXCXQXLDCCSXCNXNCV 27

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	81	67.5	26	1	US-08-496-847-19
5	81	67.5	26	2	US-08-742-774-19
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7	81	67.5	26	2	US-08-965-918-19
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9	81	67.5	26	3	US-08-613-400A-19
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21	77	64.2	26	4	US-09-392-979A-8
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23	72	60.0	25	3	US-08-899-232-3
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29	69	57.5	26	2	US-08-742-774-29	Sequence 29, Appl
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41	69	57.5	26	4	US-09-392-979A-29	Sequence 29, Appl
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43	69	57.5	25	1	US-08-185-432-17	Sequence 17, Appl
44	68	56.7	25	1	US-08-083-590A-20	Sequence 20, Appl
45	68	56.7	25	3	US-08-532-384-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-619-936-1
Sequence 1, Application US/08619936
Patent No. 5672682
GENERAL INFORMATION:
APPLICANT: Terlau, Heinrich
APPLICANT: Shon, Ki-Joon
APPLICANT: Grille, Michelle
APPLICANT: Oliveira, Balduino M.
TITLE OF INVENTION: Conotoxin Peptide PVIIA
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,936
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 24260-107674-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus purpurascens
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "4Hyp"
OTHER INFORMATION: /note= "Amino acid 4 may be 4-trans-hydroxyproline."
FEATURE:

GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Howersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipalli, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0980
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNK-202, FIGURE 2
US-08-496-847-19
Query Match 67.5%; Score 81; DB 1; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.14;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;
QY 1 CXIXNQXQXILDDCCSXKXNXXNC 26
Db 1 CKLKGSCSRIMYDCCSGSGRSGKC 26
RESULT 5
US-08-742-774-19
Sequence 19, Application US/08742774
Patent No. 5824645
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0980
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNK-202, FIGURE 2
US-08-742-774-19
Query Match 67.5%; Score 81; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.14;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;
QY 1 CXIXNQXQXILDDCCSXKXNXXNC 26
Db 1 CKLKGSCSRIMYDCCSGSGRSGKC 26
RESULT 6
US-08-675-354-19
Sequence 19, Application US/08675354
Patent No. 5859186
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794

RESULT 9
US-08-613-400A-19
; Sequence 19, Application US/08613400A
; Patent No. 6054429
; GENERAL INFORMATION:
; APPLICANT: Bowersox, S. Scott
; APPLICANT: Gaddis, Theresa
; APPLICANT: Petrus, Mark, R.
; APPLICANT: Luther, Robert, R.
; TITLE OF INVENTION: IMPROVED EPIDURAL
; TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; ZIP: 94306-1546
; COUNTRY: US
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/613,400A
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
; REGISTRATION NUMBER: 34,444
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-08-613-400A-19
Query Match 67.5%; Score 81; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.14;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

ADDRESSSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,017
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-09-298-017-19
Query Match 67.5%; Score 81; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.14;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

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1      RESULT 13
2      US-08-049-794-8
3      : Sequence 8, Application US/08049794
4      : Patent No. 5587454
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: JUSTICE, ALAN
8      : APPLICANT: SINGH, TEJINDER
9      : APPLICANT: GOHIL, KISHOR C
10     : APPLICANT: VALENTINO, KAREN L
11     : APPLICANT: MILLANICH, GEORGE P
12     : TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
13     : NUMBER OF SEQUENCES: 34
14     : CORRESPONDENCE ADDRESS:
15     : ADDRESSEE: Law Offices of Peter Dehlinger
16     : STREET: 350 Cambridge Avenue, Suite 300
17     : CITY: Palo Alto
18     :
19     : STATE: CA
20     : COUNTRY: USA
21     :
22     : ZIP: 94306
23     :
24     : COMPUTER READABLE FORM:
25     : MEDIUM TYPE: Floppy disk
26     : COMPUTER: IBM PC compatible
27     : OPERATING SYSTEM: PC-DOS/MS-DOS
28     : SOFTWARE: PatentIn Release #1.0, Version #1.25
29     :
30     : CURRENT APPLICATION DATA:
31     : APPLICATION NUMBER: US/08/049,794
32     : FILING DATE: 19930415
33     : CLASSIFICATION: 514
34     :
35     : PRIOR APPLICATION DATA:
36     : APPLICATION NUMBER: US 07/814,759
37     : FILING DATE: 30-DEC-1991
38     :
39     : ATTORNEY/AGENT INFORMATION:
40     : NAME: Stratford, Carol A.
41     : REGISTRATION NUMBER: 34,444
42     : REFERENCE/DOCKET NUMBER: 5865-0009.30
43     : TELECOMMUNICATION INFORMATION:
44     : TELEPHONE: (415) 324-0880
45     : TELEFAX: (415) 324-0960
46     :
47     : INFORMATION FOR SEQ ID NO: 8:
48     : SEQUENCE CHARACTERISTICS:
49     : LENGTH: 26 amino acids
50     : TYPE: AMINO ACID
51     : TOPOLOGY: linear
52     :
53     : MOLECULE TYPE: protein
54     :
55     : HYPOTHEetical: NO
56     :
57     : ORIGINAL SOURCE:
58     :
59     : INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
60     :
61     : US-08-049-794-8

```

APPLICANT: GORTL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPiate ANALGESIA

CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
CMBRM: 350 Cambridge Avenue, Suite 300

COUNTRY: USA
ZTD. 94306

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT AFFILIATION DATA:
APPLICATION NUMBER: US/08/742,774

CLASSIFICATION:

PRIOR APPLICATION DATA:

FILING DATE: 03-JUL-1996
APPLICATION NUMBER: IIS/08/0049

FILING DATE: 1993-APR-15

FILING DATE: 30-DEC-1991

NAME: Stratford, Carol A.

REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

MOLECULE TYPE: protein

ORIGINAL SOURCE: NO
HYPOTHETICAL: NO

INDIVIDUAL ISOLATE: SY1B/SNX-183, FIGURE 1
8-742-774-8

54 38: score 77: DB 3: Ianath 26

Best Local Similarity 34.68; Pred. No. 0.31;

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time : 15 secs
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1. The first part of the paper is devoted to the study of the properties of the function $f(x)$ defined by the equation

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 18:30:52 ; Search time 11 seconds
(without alignments)
47.621 Million cell updates/sec

Title: US-09-666-837B-1
Sequence: 1 CXIKNQXCKXILDDCCSXKXNMCV 27

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues
Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PC7_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PC7_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	56.7	2444	10 US-09-944-849-2	Sequence 2, Appl1
2	66	55.0	176	9 US-10-024-599-4	Sequence 4, Appl1
3	66	55.0	721	10 US-09-908-322-5	Sequence 5, Appl1
4	65.5	54.6	36	10 US-09-894-882-168	Sequence 168, App
5	65.5	54.6	36	10 US-09-894-882-369	Sequence 369, App
6	65.5	54.6	73	10 US-09-894-882-167	Sequence 167, App
7	64.5	53.8	32	10 US-09-894-882-364	Sequence 364, App
8	64.5	53.8	32	10 US-09-894-882-413	Sequence 413, App
9	64.5	53.8	33	10 US-09-894-882-119	Sequence 119, App
10	63.5	52.9	36	10 US-09-894-882-324	Sequence 324, App
11	63.5	52.9	36	10 US-09-894-882-339	Sequence 339, App
12	63.5	52.9	36	10 US-09-894-882-441	Sequence 441, App
13	63.5	52.9	36	10 US-09-894-882-443	Sequence 443, App
14	63.5	52.9	72	10 US-09-894-882-323	Sequence 323, App
15	63.5	52.9	72	10 US-09-894-882-338	Sequence 338, App
16	63	52.5	76	9 US-09-749-637A-207	Sequence 207, App
17	63	52.5	1055	10 US-09-855-722-2	Sequence 2, Appl1
18	63	52.5	1212	10 US-09-855-722-3	Sequence 3, Appl1
19	63	52.5	1238	10 US-09-855-722-5	Sequence 5, Appl1

20	63	52.5	1238	10 US-09-944-849-4	Sequence 4, Appl1
21	62.5	52.1	35	10 US-09-894-882-433	Sequence 433, App
22	62.5	52.1	36	10 US-09-894-882-210	Sequence 210, App
23	62.5	52.1	36	10 US-09-894-882-404	Sequence 404, App
24	62.5	52.1	70	10 US-09-894-882-209	Sequence 209, App
25	62.5	52.1	71	10 US-09-894-882-74	Sequence 74, Appl
26	62	51.7	157	10 US-09-894-882-68	Sequence 68, Appl
27	62	51.7	165	10 US-09-867-550-1550	Sequence 1550, Ap
28	62	51.7	196	10 US-09-894-882-35	Sequence 35, Appl
29	62	51.7	520	10 US-09-995-593A-3	Sequence 3, Appl1
30	62	51.7	702	10 US-09-995-593A-4	Sequence 4, Appl1
31	62	51.7	722	10 US-09-908-322-12	Sequence 12, Appl
32	62	51.7	723	9 US-10-028-072-346	Sequence 346, App
33	62	51.7	723	10 US-09-828-366-21	Sequence 21, Appl
34	62	51.7	723	10 US-09-995-593A-9	Sequence 9, Appl1
35	61.5	51.2	35	10 US-09-894-882-409	Sequence 409, App
36	61.5	51.2	36	9 US-09-814-452-25	Sequence 25, Appl
37	61.5	51.2	36	10 US-09-894-882-401	Sequence 401, App
38	61.5	51.2	36	10 US-09-894-882-403	Sequence 403, App
39	61.5	51.2	70	10 US-09-894-882-200	Sequence 200, App
40	61.5	51.2	70	10 US-09-894-882-206	Sequence 206, App
41	61.5	51.2	72	10 US-09-894-882-107	Sequence 107, App
42	61	50.8	728	10 US-09-908-322-2	Sequence 2, Appl1
43	61	50.8	1404	10 US-09-944-849-8	Sequence 8, Appl1
44	61	50.8	1480	12 US-10-011-064-5	Sequence 5, Appl1
45	61	50.8	3571	9 US-10-150-821-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-944-849-2
Sequence 2, Application US/09944849
Patent No. US20020151487A1
GENERAL INFORMATION:
APPLICANT: Nickoloff, Brian
APPLICANT: Miele, Lucio
TITLE OF INVENTION: METHOD AND REAGENTS FOR EPITHELIAL BARRIER FORMATION AND TREAT
TITLE OF INVENTION: MALIGNANT AND BENIGN SKIN DISORDERS BY MODULATING THE NOTCH P
FILE REFERENCE: 212583
CURRENT APPLICATION NUMBER: US/09/944,849
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,614
PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 2444
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (691)..(891)
OTHER INFORMATION: The 'Xaa' at location 891 stands for Gly, or Ala.
NAME/KEY: misc_feature
LOCATION: (1763)..(1763)
OTHER INFORMATION: The 'Xaa' at location 1763 stands for Gln, Arg, Pro, or Leu.
NAME/KEY: misc_feature
LOCATION: (1787)..(1787)
OTHER INFORMATION: The 'Xaa' at location 1787 stands for Thr, Ala, Pro, or Ser.
OTHER INFORMATION: Constitutively Active No. US20020151487A1ch-1
US-09-944-849-2

Query Match 56.7%; Score 68; DB 10; Length 2444;
Best local Similarity 30.8%; Pred. No. 48;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
2 CXIKNQXCKXILDDCCSXKXNMCV 27
DB 248 GFTQNCENIDDCGNNCKNGACV 273

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RESULT 2
US-10-024-599-4
: Sequence 4, Application US/10024599
: Patent No. US20020165352A1
: GENERAL INFORMATION:
: APPLICANT: Myriad Genetics, Inc.
: APPLICANT: Cimborra, Daniel M.
: APPLICANT: Heichman, Karen
: APPLICANT: Bartel, Paul L.
: TITLE OF INVENTION: Protein-Protein Interactions
: FILE REFERENCE: 2318-278-II
: CURRENT APPLICATION NUMBER: US/10/024-599
: PRIOR FILING DATE: 2001-12-21
: PRIOR APPLICATION NUMBER: US 60/256,986
: PRIOR FILING DATE: 2000-12-21
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 4
: LENGTH: 176
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: PEPTIDE
: LOCATION: 1..176
: OTHER INFORMATION: Xaa is Gly or Cys
US-10-024-599-4

Query Match          55.0%; Score 66; DB 9; Length 176;
Best Local Similarity 25.8%; Pred. No. 6.6;
Matches      8; Conservative 14; Mismatches      5; Indels      4; Gaps      1.

OY      1 CXIXN---QXCXQLDDCCSXKXKXNXCXV 27
: 1: 1 :1:::111 :1 :1:::1:
Db      9 CVCVNGSGDCCSENIDCCAFACCTGGSYCI 39

RESULT 3
US-09-308-322-5
: Sequence 5, Application US/09908322
: Patent No. US20020107194A1
: GENERAL INFORMATION:
: APPLICANT: Ish-Horowicz, David
: Henriquez, Domingos Manuel Pinto
: Lewis, Julian Hart
: Artavanis-Tsakonas, Spyridon
: Gray, Grace
: TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
: VERTEBRATE DELTA GENE AND METHODS BASED THEREON
: NUMBER OF SEQUENCES: 94
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennile & Edmonds LLP
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10036/2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/908,322
: FILING DATE: 17-Jul-2001
: CLASSIFICATION: <unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/981,392
: FILING DATE: 22-DEC-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Mastrock, S Leslie
: REGISTRATION NUMBER: 18,872
: REFERENCE/DOCKET NUMBER: 7326-123
: TELECOMMUNICATION INFORMATION:

```

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      TELEPHONE: 212-790-9090
      TELEFAX: 212-869-8864
      TELEX: 66141 PENNIE
      INFORMATION FOR SEQ ID NO: 5:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 721 amino acids
          TYPE: amino acid
          STRANDEDNESS: <Unknown>
          TOPOLOGY: unknown
        MOLECULE TYPE: peptide
      US-09-908-322-5

Query Match           55.0%; Score 66; DB 10; Length 721;
Best Local Similarity 32.0%; Pred. No. 24;
Matches      8; Conservative    11; Mismatches      6; Indels     0; Gaps     0;

QY       2 XIXNQXCXOXLDCCSXKCNXXNC 26
Db        436 GFSGRNCDDNLDCSTSPCNGTIC 460
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RESULT 4
US-09-894-882-168
; Sequence 168, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Eisle C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Oliveira, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIORITY FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 168
; LENGTH: 36
; TYPE: PRP
; ORGANISM: Conus betulinus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1..36)
; OTHER INFORMATION: Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at residues
; OTHER INFORMATION: , 23 and 36 is Tyr, 125I-Tyr, mono-Iodo-Tyr, di-Iodo-Tyr, O-su
; OTHER INFORMATION: O-Tyr or O-phospho-Ty
US-09-894-882-168

Query Match           54.6%; Score 65.5; DB 10; Length 36;
Best Local Similarity 44.4%; Pred. No. 1.7;
Matches     12; Conservative     9; Mismatches      5; Indels     1; Gaps     1;

QY       1 CXIXNQCXOXLDCCSXKCNXXNCV 27
Db         2 CLSLGQRCKRH-SDCCGXLCFCFXDKCV 27

```


Page 3

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PRIORITY FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 508
SOFTWARE: PatentIn version 3.0
SEQ ID NO 167
LENGTH: 73
TYPE: PRT
ORGANISM: Conus betulinus
US-09-894-882-167

Query Match
Best Local Similarity 54.6%; Score 65.5; DB 10; Length 73;
Matches 9; Conservative 12; Mismatches 5; Indels 1; Gaps 1;

1 CXIXNQXCXOXLDCCSXKXNXXNKCV 27
| : | : | : | | | : | : | : | : | |
Db 39 CLSIGRCERH-SDCGYLCIFYDKCV 64

RESULT 7
US-09-894-882-364
Sequence 364, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma B.
APPLICANT: Jimenez, Elsie C.
APPLICANT: McInosh, J. Michael
APPLICANT: Oliveira, Baldomero M.
APPLICANT: Watkins, Karen
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OR INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 364
LENGTH: 32
TYPE: PRT
ORGANISM: Conus bruneus
US-09-894-882-364

Query Match
Best Local Similarity 53.8%; Score 64.5; DB 10; Length 32;
Matches 9; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

1 CXIXNQXCXOXLDCCSXKXNXXNKCV 27
| : | : | : | | | : | : | : | : | |
Db 1 CGYVGQACDD-SDCGSIICVAGECV 26

RESULT 8
US-09-894-882-413
Sequence 413, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
```

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> ORGANISM: Conus magus
> US-09-894-882-119
>
> Query Match
> Best Local Similarity 33.3%; Pred. No. 3.9;
> Matches 9; Conservative 11; Mismatches 6; Indels 1; Gaps 1;
>
> OY 1 CXINQXGXLDGCCSXKXNXXNV 27
> |:::|:::|:::|:::|:::|:::|
> Db 39 CSLLGQRCSDH-SDCCMDMCASEKCY 64
>
> RESULT 10
> US-09-894-882-324
> Sequence 324 Application US/09894882
> Patent No. US20020102607A1
> GENERAL INFORMATION:
> APPLICANT: University of Utah Research Foundation
> APPLICANT: Cognetix, Inc.
> APPLICANT: Walker, Craig S.
> APPLICANT: Shetty, Reshma
> APPLICANT: Jimenez, J. Michael
> APPLICANT: Kincosh, J.
> APPLICANT: Olvera, Baldomero M.
> APPLICANT: Watkins, Maren
> APPLICANT: Jones, Robert M.
> APPLICANT: Shen, Greg S.
> TITLE OF INVENTION: 1-Superfamily Conotoxins
> FILE REFERENCE: 2314-238
> CURRENT APPLICATION NUMBER: US/09/894,882
> CURRENT FILING DATE: 2001-06-29
> PRIOR APPLICATION NUMBER: US 60/
> PRIOR FILING DATE: 2000-06-30
> PRIOR APPLICATION NUMBER: US 60/243,410
> PRIOR FILING DATE: 2000-10-27
> PRIOR APPLICATION NUMBER: US 60/246,581
> PRIOR FILING DATE: 2000-11-08
> PRIOR APPLICATION NUMBER: US 60/247,714
> PRIOR FILING DATE: 2000-11-14
> PRIOR APPLICATION NUMBER: US 60/264,256
> PRIOR FILING DATE: 2001-01-29
> NUMBER OF SEQ ID NOS: 506
> SOFTWARE: PatentIn version 3.0
> SEQ ID NO 324
> LENGTH: 36
> TYPE: PRT
> ORGANISM: Conus episcopatus
> FEATURE:
> NAME/KEY: PEPTIDE
> LOCATION: (1)..(36)
> OTHER INFORMATION: Xaa at residue 36 is Pro or hydroxy-Pro; Xaa at residue 23 is
> OTHER INFORMATION: 1,121-Tyr, mono-Iodo-Tyr, di-Iodo-Tyr, O-sulpho-Tyr or O-phos
> US-09-894-882-324
>
> Query Match
> Best Local Similarity 52.9%; Score 63.5; DB 10; Length 36;
> Matches 10; Conservative 9; Mismatches 6; Indels 1; Gaps 1;
>
> OY 1 CXINQXGXLDGCCSXKXNXXNC 26
> |:::|:::|:::|:::|:::|:::|
> Db 3 CSRIQGCCGD-SDCCDMDCKXGIC 27
>
> RESULT 11
> US-09-894-882-339
> Sequence 339 Application US/09894882
> Patent No. US20020102607A1
> GENERAL INFORMATION:
> APPLICANT: University of Utah Research Foundation
> APPLICANT: Cognetix, Inc.
> APPLICANT: Walker, Craig S.
> APPLICANT: Shetty, Reshma

```

RESULT 12
US-09-894-882-441
Sequence 441, Application US/0984882
Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Karen
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 441

APPLICANT: Watkins, Maren

```
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 323
LENGTH: 72
TYPE: PRT
ORGANISM: Conus episcopatus
US-09-894-882-323
```

```
Query Match          52.9%; Score 63.5; DB 10; Length 72;
Best Local Similarity 34.6%; Pred. No. 4.9;
Matches 9; Conservative 10; Mismatches 6; Indels 1; Gaps 1;
```

```
OY      1 CXIXNQXCXQXLDCCSXNCXNXC 26
       |: :|:|:|: ||| :|:|:|:|
Db      39 CSRIGGCGGD-SPCCGDMCCHGQIC 63
```

```
RESULT 15
US-09-894-882-338
Sequence 338, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 338
LENGTH: 72
TYPE: PRT
ORGANISM: Conus episcopatus
US-09-894-882-338
```

```
Query Match          52.9%; Score 63.5; DB 10; Length 72;
Best Local Similarity 34.6%; Pred. No. 4.9;
Matches 9; Conservative 10; Mismatches 6; Indels 1; Gaps 1;
```

```
OY      1 CXIXNQXCXQXLDCCSXNCXNXC 26
       |: :|:|:|: ||| :|:|:|:|
Db      39 CSRIGGCGGD-SPCCGDMCCHGQIC 63
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Search completed: January 14, 2003, 18:32:41
Job time : 12 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2003, 18:29:51 ; Search time 16 Seconds
(without alignments)
162.227 Million cell updates/sec

Title: US-09-666-837b-1
Perfect score: 120
Sequence: 1 CXIXNQKXQXLDLDCSXKXNKNXCV 27

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR-73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	100.0	27	2	A58997 kappa-conotoxin PV
2	77	64.2	26	2	C44379 omega-conotoxin SV
3	72	60.0	2524	2	A35844 Notch protein - Af
4	69	57.5	29	2	UHO699 omega-conotoxin MV
5	68	56.7	2555	2	A40043 Notch protein homo
6	67	55.8	293	2	B26637 neurogenic repetit
7	67	55.8	2139	2	A35672 crumb protein - f
8	67	55.8	2437	2	S42612 transmembrane prot
9	67	55.8	2531	2	S18188 Notch protein homo
10	67	55.8	2531	2	A46019 Notch-1 protein -
11	66	55.0	29	2	B43620 omega-conotoxin GV
12	66	55.0	1203	2	A49175 Notch B protein -
13	66	55.0	2471	2	A49128 cell-fate determin
14	66	55.0	2703	1	A24420 Notch protein - fir
15	65	54.2	601	2	T22025 hypothetical prote
16	65	54.2	601	2	D89711 protein F40E10.4 l
17	65	54.2	1964	2	T09059 Notch4 - mouse
18	65	54.2	2318	2	S45306 Notch 3 protein -
19	65	54.2	2321	2	S78549 Notch3 protein - h
20	65	54.2	2531	2	T31070 Notch homolog - se
21	64	53.3	1372	2	T25933 hypothetical prote
22	64	53.3	2352	2	T30201 Notch homolog prot
23	64	53.3	3623	2	T08618 Notch factor-B
24	63	52.5	43	2	S18174 metallothionein -
25	63	52.5	570	2	A48836 fibropellin C prec
26	63	52.5	1687	2	T30176 EGF repeat transme
27	62	51.7	29	2	A43620 omega-conotoxin GV
28	62	51.7	722	2	I48324 DELTA-like 1 - mou
29	62	51.7	1064	2	A40136 fibropellin Ia - s

30	61.5	51.2	36	1	A32038 mu-agatoxin I - fu
31	61	50.8	29	2	A58537 omega-conotoxin MV
32	61	50.8	728	2	C-Delta-1 - Chloke
33	61	50.8	1025	2	T42626 secreted leucine-r
34	61	50.8	1408	2	S16148 gene serrate prote
35	61	50.8	1469	2	B36655 slit protein 2 pre
36	61	50.8	1480	2	A36655 slit protein 1 pre
37	60	50.0	354	2	T22274 hypothetical prote
38	60	50.0	832	2	A31246 neurogenic protein
39	60	50.0	833	2	S19087 gene Delta protein
40	60	50.0	880	2	S00670 neurogenic repetit
41	60	50.0	1295	2	A32901 glp1 protein precu
42	60	50.0	1722	2	E89753 protein FILC7.4 l
43	59	49.2	25	2	JH0701 omega-conotoxin MV
44	59	49.2	43	2	S18173 metallothionein -
45	59	49.2	43	2	S33382 metallothionein -

ALIGNMENTS

RESULT 1

A58997 kappa-conotoxin PV1A - cone shell (Conus purpurascens)
N:Alternate names: fin-popping peptide
C:Species: Conus purpurascens (purple cone)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C:Accession: A58997
R:Terlau, H.; Shon, K.J.; Grilley, M.; Stocker, M.; Stuehmer, W.; Olivera, B.M.
Nature 381, 148-151, 1996
A:Title: Strategy for rapid immobilization of prey by a fish-hunting marine snail.
A:Reference number: A58997
A:Accession: A58997
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-27 <TRP>
C:Comment: This conotoxin blocks conductance of the Shaker potassium channel.
C:Keywords: hydroxyproline; neurotoxin; venom
F:4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 100.0%; Score 120; DB 2; Length 27;
Best local Similarity 63.0%; Pred. No. 4.3e-05;
Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXIXNQKXQXLDLDCSXKXNKNXCV 27
DB 1 CRIPNQKCFHLDLDCSRKCNREKVCV 27

RESULT 2

C44379 omega-conotoxin SV1B [validated] - cone shell (Conus striatus)
N:Alternate names: SNK-183
C:Species: Conus striatus (striated cone)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Sep-2000
C:Accession: C44379
R:Ramilo, C.A.; Zafaralla, G.C.; Nadasdi, L.; Hammerland, L.G.; Yoshikami, D.; Gray, R.
Biochemistry 31, 9919-9926, 1992
A:Title: Novel alpha- and omega-conotoxins from Conus striatus venom.
A:Reference number: A44379; MUID:93003172; PMID:1390774
A:Accession: C44379
A:Molecule type: protein
A:Residues: 1-26 <RAM>
A:Cross-references: CAS:143306-19-8
A:Experimental source: venom
A>Note: sequence extracted from NCBI backbone (NCBI:116002); structure confirmed by submitted to the Brookhaven Protein Data Bank, August 1996
R:Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
A:Reference number: A67649; PDB:1MY7
A:Contents: annotation; conformation by (1)H-NMR, residues 1-26
R:Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
J. Mol. Biol. 263, 297-310, 1996
A:Title: A consensus structure for omega-conotoxins with different selectivities for

A:Reference number: A58619; MUID:97070382; PMID:8913308
A:Contents: annotation: conformation by (1)H-NMR
C:Comment: This omega-conotoxin blocks presynaptic calcium channels.
C:Superfamily: omega-conotoxin
C:Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh
F:1-16,8-20,15-26/Disulfide bonds: #status predicted
F:26/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 64.2%; Score 77; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.42;
Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

OY 1 CXIXNOCXOXLDCCSXXCNXXNXC 26
DB 1 CKIKGSCRKISYDCSGSGCRGKC 26

RESULT 3
A35844
Xotch protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 02-Aug-2002
C:Accession: A35844
R:Coffman, C.; Harris, W.; Kintner, C.
Science 249, 1438-1441, 1990
A:Title: Xotch, the Xenopus homolog of Drosophila notch.
A:Reference number: A35844; MUID:90385285; PMID:2402639
A:Accession: A35844
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-2524 <COE>
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
C:Keywords: transmembrane protein
F:146-177/Domain: EGF homology <EGF1>
F:184-215/Domain: EGF homology <EGF1>
F:222-254/Domain: EGF homology <EGF1>
F:456-487/Domain: EGF homology <EGF2>
F:57-788/Domain: EGF homology <EGF3>
F:1025-1056/Domain: EGF homology <EGF3>
F:1924-1956/Domain: ankyrin repeat homology <AN1>
F:1924-1956/Domain: ankyrin repeat homology <AN2>
F:1957-1989/Domain: ankyrin repeat homology <AN2>
F:1991-2023/Domain: ankyrin repeat homology <AN2>
F:2024-2056/Domain: ankyrin repeat homology <AN2>
F:2057-2089/Domain: ankyrin repeat homology <AN2>

Query Match 60.0%; Score 72; DB 2; Length 2524;
Best Local Similarity 34.6%; Pred. No. 27;
Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

OY 2 XIXNOCXOXLDCCSXXCNXXNXC 27
DB 248 GFGONCEINIDCPGNNCKNGACV 273

RESULT 4
JH0699
omega-conotoxin MVIC precursor [validated] - cone shell (Conus magus) (fragment)
C:Species: Conus magus (magus cone)
C:Date: 17-Apr-1993 #sequence_revision 11-Apr-1997 #text_change 15-Sep-2000
C:Accession: JH0699; PC2380
R:Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramchandran, J.; M
Neuron 9, 69-77, 1992
A:Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.
A:Reference number: JH0699; MUID:92337922; PMID:1352986
A:Accession: JH0699
A:Molecule type: mRNA
A:Residues: 1-29 <HIL>
A:Cross-references: GB:S40826; NID:9252126; PIDN:AA822674.1; PID:9252127
R:Nemoto, N.; Kubo, S.; Yoshida, T.; Chino, N.; Kimura, T.; Sakakibara, S.; Kyogoku, Y.;
Biochem. Biophys. Res. Commun. 207, 695-700, 1995
A:Title: Solution structure of omega-conotoxin MVIC determined by NMR.
A:Reference number: PC2380; MUID:95169113; PMID:7864862
A:Accession: PC2380

A:Molecule type: protein
A:Residues: 3-28 <NEM>
R:Farr-Jones, S.; Basus, V.J.
submitted to the Brookhaven Protein Data Bank, December 1994
A:Reference number: A66297; PDB:1OMN
A:Contents: annotation: conformation by (1)H-NMR, residues 3-28
R:Farr-Jones, S.; Miljanich, G.P.; Nadasdi, L.; Ramchandran, J.; Basus, V.J.
J. Mol. Biol. 248, 106-124, 1995
A:Title: Solution structure of omega-conotoxin MVIC, a high affinity of P-type calci
A:Reference number: A58582; MUID:95248539; PMID:7731037
A:Contents: annotation: conformation by (1)H-NMR
C:Superfamily: omega-conotoxin
C:Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel
F:3-28/Product: omega-conotoxin MVIC #status experimental <MAH>
F:3-18,10-22,17-28/Disulfide bonds: #status experimental
F:28/Modified site: amidated carboxyl end (Cys) (amide in mature form from following

Query Match 57.5%; Score 69; DB 2; Length 29;
Best Local Similarity 30.8%; Pred. No. 2.5;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

OY 1 CXIXNOCXOXLDCCSXXCNXXNXC 26
DB 3 CKKGAPCRKTYDCSGSGCRGKC 28

RESULT 5
A40043
Notch protein homolog TAN-1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 02-Aug-2002
C:Accession: A40043
R:Eilissen, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, T.C.; Smith, S.D.; SKI
Cell 66, 649-661, 1991
A:Title: TAN-1, the human homolog of the Drosophila Notch gene, is broken by chromoso
A:Reference number: A40043; MUID:91347367; PMID:1871692
A:Accession: A40043
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:Molecule type: mRNA
A:Residues: 1-2555 <EIL>
A:Cross-references: GB:M73980
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:261-292/Domain: EGF homology <EGF1>
F:494-525/Domain: EGF homology <EGF1>
F:987-1018/Domain: EGF homology <EGF2>
F:1149-1180/Domain: EGF homology <EGF2>
F:1187-1218/Domain: EGF homology <EGF3>
F:1233-1264/Domain: EGF homology <EGF3>
F:1927-1959/Domain: ankyrin repeat homology <AN1>
F:1960-1992/Domain: ankyrin repeat homology <AN1>
F:1994-2026/Domain: ankyrin repeat homology <AN1>
F:2027-2059/Domain: ankyrin repeat homology <AN1>
F:2060-2092/Domain: ankyrin repeat homology <AN1>

Query Match 56.7%; Score 68; DB 2; Length 2555;
Best Local Similarity 30.8%; Pred. No. 63;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

OY 2 XIXNOCXOXLDCCSXXCNXXNXC 27
DB 248 GFGONCEINIDCPGNNCKNGACV 273

RESULT 6
B26637
neurogenic repetitive locus 95F protein - fruit fly (Drosophila melanogaster) (fragme
C:Species: Drosophila melanogaster
C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 21-Jul-2000
C:Accession: B26637
R:Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigelt, D.; Vaesslin, H.; Campos-
EMBO J. 6, 761-766, 1987
A:Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster. a
A:Reference number: A31081; MUID:87218537; PMID:3107966

A:Accession: B26637
 A:Molecule type: mRNA
 A:Residues: 1-293 <KNV>
 A:Cross-references: GB:X05144; MID:97519; PIDN:CAA28793.1; PID:929536
 C:Genetics:
 A:Gene: FLYBase:crb
 A:Cross-references: FLYBase:FBgn0000368
 C:Superfamily: unassigned EGF-related proteins; EGF homology
 C:Keywords: Transmembrane protein
 F:139-170/Domain: EGF homology <EGX1>
 F:177-208/Domain: EGF homology <EGF1>
 F:216-252/Domain: EGF homology <EGF>

Query Match 55.8%; Score 67; DB 2; Length 293;
 Best Local Similarity 28.0%; Pred. No. 18;
 Matches 7; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

OY 2 XIXNXXCXQXLDCCSXCNXXNC 26
 Db 164 GFEGQHCEQNDICADQPCNHGNC 188

RESULT 7
 A35672
 crumbs protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 21-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 11-Jan-2000
 C:Accession: A35672
 R:Teppas, U.; Theres, C.; Knust, E.
 Cell 61, 787-799, 1990
 A:Title: crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila
 A:Reference number: A35672; MID:90263104; PMID:2344615
 A:Accession: A35672
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2139 <TEP>
 A:Cross-references: GB:M33753
 A:Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residue
 C:Genetics:
 A:Gene: FLYBase:crb
 A:Cross-references: FLYBase:FBgn0000368
 C:Superfamily: unassigned EGF-related proteins; EGF homology
 C:Keywords: Transmembrane protein
 F:352-385/Domain: EGF homology <EGX1>
 F:392-424/Domain: EGF homology <EGF1>
 F:691-722/Domain: EGF homology <EGF>
 F:767-799/Domain: EGF homology <EGF3>
 F:1878-1914/Domain: EGF homology <EGX2>

Query Match 55.8%; Score 67; DB 2; Length 2139;
 Best Local Similarity 28.0%; Pred. No. 70;
 Matches 7; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

OY 2 XIXNXXCXQXLDCCSXCNXXNC 26
 Db 1826 GFEGQHCEQNDICADQPCNHGNC 1850

RESULT 8
 S42612
 Transmembrane protein precursor - zebra fish
 C:Species: Brachydanio rerio (zebra fish)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002
 C:Accession: S42612
 R:Bierkamp, C.; Campos-Ortega, J.A.
 Mech. Dev. 43, 87-100, 1993
 A:Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern
 A:Reference number: S42612; MID:94128602; PMID:8237791
 A:Accession: S42612
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2437 <BTE>
 A:Cross-references: EMBL:X69088; MID:9433866; PIDN:CAA48931.1; PID:9433867

C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
 F:755-786/Domain: EGF homology <EGF1>
 F:1023-1054/Domain: EGF homology <EGF1>
 F:1185-1216/Domain: EGF homology <EGF2>
 F:1915-1947/Domain: ankyrin repeat homology <AN1>
 F:1948-1980/Domain: ankyrin repeat homology <AN2>
 F:1982-2014/Domain: ankyrin repeat homology <AN3>
 F:2015-2047/Domain: ankyrin repeat homology <AN4>
 F:2048-2080/Domain: ankyrin repeat homology <AN5>

Query Match 55.8%; Score 67; DB 2; Length 2437;
 Best Local Similarity 30.0%; Pred. No. 76;
 Matches 9; Conservative 13; Mismatches 4; Indels 4; Gaps 1;

OY 1 CXIXN---QXCXQXLDCCSXCNXXNC 26
 Db 320 CVCVNGWGTGDCSENIIDCASACSHGATC 349

RESULT 9
 S1818
 notch protein homolog - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
 C:Accession: S1818
 R:Weinmaster, G.; Roberts, V.J.; Lemke, G.
 Development 113, 199-205, 1991
 A:Title: A homolog of Drosophila Notch expressed during mammalian development.
 A:Reference number: S18188; MID:92111383; PMID:1764995
 A:Accession: S18188
 A:Molecule type: mRNA
 A:Residues: 1-2531 <WEI>
 A:Cross-references: EMBL:X57405; MID:957634; PID:957635
 C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
 F:987-1018/Domain: EGF homology <EGF1>
 F:1025-1056/Domain: EGF homology <EGF2>
 F:1233-1264/Domain: EGF homology <EGF2>
 F:1917-1949/Domain: ankyrin repeat homology <AN1>
 F:1950-1982/Domain: ankyrin repeat homology <AN2>
 F:1984-2016/Domain: ankyrin repeat homology <AN3>
 F:2017-2049/Domain: ankyrin repeat homology <AN4>
 F:2050-2082/Domain: ankyrin repeat homology <AN5>

Query Match 55.8%; Score 67; DB 2; Length 2531;
 Best Local Similarity 30.8%; Pred. No. 78;
 Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

OY 2 XIXNXXCXQXLDCCSXCNXXNCV 27
 Db 248 GFAGQNCENVDPCGNCKNGACV 273

RESULT 10
 A46019
 Notch-1 protein - mouse
 N:Alternate names: notch protein
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Sep-1999
 C:Accession: A46019; S25144
 R:del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; G
 Genomics 15, 259-264, 1993
 A:Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog
 A:Reference number: A46019; MID:93194170; PMID:8449489
 A:Accession: A46019
 A:Status: not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-2531 <DEI>
 A:Cross-references: GB:J11886; GB:S47228; MID:9288502; PIDN:CAA77941.1; PID:9288503
 A:Note: sequence extracted from NCBI backbone (NCBI:P:127318)
 R:Francisco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J
 submitted to the EMBL Data Library, April 1992
 A:Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, sugg

A:Accession: S25144
A:Molecule type: mRNA
A:Residues: 1551-2108, 'Q', 2110-2114, 'ALP', 2118-2170 <FRA>
A:Cross-references: EMBL:Z11886
C:Genetics:
A:Gene: notch-1
A:Map position: 2
A>Note: proximal region of chromosome 2
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
F:106-138/Domain: EGF homology <EGF1>
F:144-175/Domain: EGF homology <EGF1>
F:222-254/Domain: EGF homology <EGF2>
F:261-292/Domain: EGF homology <EGF2>
F:339-370/Domain: EGF homology <EGF3>
F:416-449/Domain: EGF homology <EGF3>
F:456-487/Domain: EGF homology <EGF4>
F:534-555/Domain: EGF homology <EGF5>
F:532-563/Domain: EGF homology <EGF6>
F:607-638/Domain: EGF homology <EGF7>
F:682-713/Domain: EGF homology <EGF8>
F:757-788/Domain: EGF homology <EGF9>
F:795-826/Domain: EGF homology <EGF10>
F:873-904/Domain: EGF homology <EGF11>
F:911-942/Domain: EGF homology <EGF12>
F:949-980/Domain: EGF homology <EGF13>
F:987-1018/Domain: EGF homology <EGF14>
F:1025-1056/Domain: EGF homology <EGF15>
F:1063-1094/Domain: EGF homology <EGF16>
F:1149-1180/Domain: EGF homology <EGF17>
F:1187-1218/Domain: EGF homology <EGF18>
F:1233-1264/Domain: EGF homology <EGF19>
F:1352-1383/Domain: EGF homology <EGF19>
F:1391-1425/Domain: EGF homology <EGF19>
F:1917-1948/Domain: ankyrin repeat homology <AN1>
F:1949-1981/Domain: ankyrin repeat homology <AN2>
F:1983-2015/Domain: ankyrin repeat homology <AN3>
F:2016-2048/Domain: ankyrin repeat homology <AN4>
F:2049-2081/Domain: ankyrin repeat homology <AN5>

Query Match 55.8%; Score 67; DB 2; Length 2531;
Best Local Similarity 30.8%; Pred. No. 78;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNXQXQXLDCCSXKXNXCXCV 27
Db 248 GFAGQCEENVDCPGNCKNGACV 273

RESULT 11
B43620
Omega-conotoxin CVIIR - cone shell (Conus geographus)
N:Alternate names: Shaker peptide GV11B
C:Species: Conus geographus (geography cone)
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 23-May-1997
C:Accession: B43620
R:OLivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Santis
Science 230, 1338-1343, 1985
A:Title: Peptide neurotoxins from fish-hunting cone snails.
A:Reference number: A43620; MUID:86070213; PMID:4071055
A:Accession: B43620
A:Molecule type: protein
A:Residues: 1-29 <OLI>
C:Superfamily: omega-conotoxin
C:Keywords: acetylcholine release inhibition; calcium channel inhibitor; hydroxyproline;
F:1-16-8-19-15-26/disulfide bonds; #status predicted
F:4,7/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 55.0%; Score 66; DB 2; Length 29;
Best Local Similarity 26.9%; Pred. No. 4.8;
Matches 7; Conservative 14; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXIXNXQXQXLDCCSXKXNXCXCV 26
Db 1 CXIXNXQXQXLDCCSXKXNXCXCV 26

Db 1 CKSPGFCRGMRDCTCSLSTSYNKC 26

RESULT 12
A49175
Notch B protein - mouse (fragment)
N:Alternate names: Notch homolog
C:Species: Mus musculus (house mouse)
C:Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 20-Sep-1999
C:Accession: A49175; PMID:93170; S32113
R:Cardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A:Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety
A:Reference number: A49175; MUID:93170563; PMID:8440332
A:Accession: A49175
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1203 <LAR>
A:Cross-references: EMBL:X68279; NID:g287989; PIDN:CAA48340.1; PID:g287990
A:Experimental source: embryo
A>Note: sequence extracted from NCBI backbone (NCBI:126158)
C:Comment: This protein has many EGF repeats and 11n-12/Notch repeats.
C:Comment: This protein is one of the neurogenic proteins controlling the decision be
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol
F:143-174/Domain: EGF homology <EGX1>
F:482-513/Domain: EGF homology <EGF1>
F:560-591/Domain: EGF homology <EGF>
F:674-705/Domain: EGF homology <EGX2>
F:712-743/Domain: EGF homology <EGF3>
F:836-867/Domain: EGF homology <EGX3>

Query Match 55.0%; Score 66; DB 2; Length 1203;
Best Local Similarity 25.8%; Pred. No. 59;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

QY 1 CXIXN----QXQXQXLDCCSXKXNXCXCV 27
Db 7 CVCVNGMSGDCSENIDDCAYASCTPGSTCI 37

RESULT 13
A49128
cell-fate determining gene Notch2 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002
C:Accession: A49128
R:Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development 116, 931-941, 1992
A:Title: Notch2: a second mammalian Notch gene.
A:Reference number: A49128; MUID:93202015; PMID:1295745
A:Accession: A49128
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2471 <WEI>
A:Experimental source: Schwann cell
A>Note: sequence extracted from NCBI backbone (NCBI:127811)
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:264-295/Domain: EGF homology <EGX1>
F:799-830/Domain: EGF homology <EGF1>
F:877-908/Domain: EGF homology <EGX2>
F:1029-1060/Domain: EGF homology <EGF>
F:1067-1098/Domain: EGF homology <EGF3>
F:1153-1184/Domain: EGF homology <EGF3>
F:1191-1222/Domain: EGF homology <EGF3>
F:1676-1908/Domain: ankyrin repeat homology <EGX4>
F:1909-1941/Domain: ankyrin repeat homology <AN1>
F:1943-1975/Domain: ankyrin repeat homology <AN2>
F:1976-2008/Domain: ankyrin repeat homology <AN4>
F:2009-2041/Domain: ankyrin repeat homology <AN5>

Query Match 55.0%; Score 66; DB 2; Length 2471;
Best Local Similarity 25.0%; Pred. No. 95;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

OY 1 CXIXN-----QXGXLDCCSXKXNXXCV 27
 DB 324 CVCXNGMSGDDCSENIDDCAFASCTPGSTCT 354

RESULT 14

A24420
 notch protein - fruit fly (Drosophila melanogaster)

N:Alternate names: neurogenic repetitive locus protein

C:Species: Drosophila melanogaster

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A24420; A24768; S09358; A05267

R:Kidd, S.; Kelley, M.R.; Young, M.W.

Mol. Cell. Biol. 6, 3094-3108, 1986

A:Reference number: A24420; M0ID:87064624; PMID:3097517

A:Accession: A24420

A:Molecule type: DNA

A:Residues: 1-2703 <KID>

A:Cross-references: GB:K03508; NID:9157991; PIDN:AAA28725.1; PID:9157993

R:Bartron, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.

Cell 43, 567-581, 1985

A:Reference number: A24768; M0ID:86079539; PMID:3935325

A:Accession: A24768

A:Molecule type: mRNA

A:Residues: 1-48, 'I', 50-118, 'R', 120-230, 'I', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-958,

A>Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044

R:Paulz, D.

Nucleic Acids Res. 17, 6463-6471, 1989

A:Title: Hypervariability of simple sequences as a general source for polymorphic DNA mo

A:Reference number: S09358; M0ID:89385974; PMID:2780284

A:Accession: S09358

A:Molecule type: DNA

A:Residues: 2505-2551, 'QCCQ', 2552-2576, 'E', 2578-2604 <TAU>

R:Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.

Cell 40, 55-62, 1985

A:Title: opa: a novel family of transcribed repeats shared by the Notch locus and other.

A:Reference number: A05267; M0ID:85099329; PMID:2981631

A:Accession: A05267

A:Molecule type: DNA

A:Residues: 2504-2576, 'E', 2578-2611 <WHA>

A:Genetics:

A:Gene: notch; opa

A:Cross-references: FlyBase:FBgn0004647

A:Map position: 8.96-9.36

A:Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 233/3; 2436/3; 2588/3

C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

C:Keywords: differentiation; tandem repeat; transmembrane protein

F:27-43/Domain: transmembrane #status predicted <TMM1>

F:297-328/Domain: EGF homology <EGX1>

F:530-561/Domain: EGF homology <EGF1>

F:568-599/Domain: EGF homology <EGF>

F:988-1019/Domain: EGF homology <EGX2>

F:1064-1095/Domain: EGF homology <EGF3>

F:1187-1218/Domain: EGF homology <EGX3>

F:1746-1762/Domain: transmembrane #status predicted <TMM2>

F:1950-1982/Domain: ankyrin repeat homology <AN1>

F:1983-2015/Domain: ankyrin repeat homology <AN2>

F:1988-2004/Domain: transmembrane #status predicted <TMM3>

F:2017-2049/Domain: ankyrin repeat homology <AN3>

F:2050-2082/Domain: ankyrin repeat homology <AN4>

F:2083-2115/Domain: ankyrin repeat homology <AN5>

F:2538-2568/Region: glutamine-rich

F:2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>

Query Match 55.0%; Score 66; DB 1; Length 2703;
 Best Local Similarity 29.2%; Pred. No. 1e+02;
 Matches 7; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

OY 4 XNXXCXOXLDCCSXKXNXXCV 27
 DB 822 TGQKCFNIDDCVTPNCGNGCTCI 845

RESULT 15

T22025
 hypothetical protein F40E10.4 - Caenorhabditis elegans (fragment)

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T22025

R:Smey, R.

submitted to the EMBL Data Library, February 1996

A:Reference number: Z19503

A:Accession: T22025

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-601 <WIL>

A:Cross-references: EMBL:Z69792; PIDN:CAA93668.1; GSPDB:GN00028; CESP:F40E10.4

A:Experimental source: clone F40E10

C:Genetics:

A:Gene: CESP:F40E10.4

A:Map position: X

Query Match 54.2%; Score 65; DB 2; Length 601;
 Best Local Similarity 26.9%; Pred. No. 46;
 Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

OY 2 XIXNXXCXOXLDCCSXKXNXXCV 27
 DB 114 GFGDYCEKRNIDDCVNSKENGKCV 139

Search completed: January 14, 2003, 18:32:03
 Job time: 18 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 18:29:11 ; Search time 11 Seconds
(without alignments)
101.806 Million cell updates/sec

Title: US-09-666-837B-1

Perfect score: 120
Sequence: 1 CXTXNQCKQXKXIDCCSXKXCNXNCV 27

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	72	1	CKX7_CONPU
2	77	64.2	72	1	CKOB_CONST
3	73	60.8	26	1	CKOC_CONCT
4	72	60.0	2524	1	NOTC_XENIA
5	69	57.5	29	1	CKOC_CONMA
6	68	56.7	2556	1	NTC1_HUMAN
7	67	55.8	2139	1	CRB_DROME
8	67	55.8	2437	1	NTC1_BRAE
9	67	55.8	2531	1	NTC1_MOUSE
10	67	55.8	2531	1	NTC1_MOUSE
11	66	55.0	2470	1	NTC2_MOUSE
12	66	55.0	2471	1	NTC2_HUMAN
13	66	55.0	2471	1	NTC2_MOUSE
14	66	55.0	2703	1	NOTC_DROME
15	65	54.2	1964	1	NTC4_MOUSE
16	65	54.2	2319	1	NTC3_HUMAN
17	65	54.2	2321	1	NTC3_MOUSE
18	65	54.2	2321	1	NTC4_HUMAN
19	64	53.3	2003	1	MTB_COLVI
20	63	52.5	43	1	MTB_COLVI
21	63	52.5	570	1	FBP3_STRPU
22	63	52.5	589	1	DLI3_RAT
23	63	52.5	592	1	DLI3_MOUSE
24	63	52.5	618	1	JAG2_HUMAN
25	63	52.5	1202	1	JAG2_MOUSE
26	63	52.5	1236	1	JAG2_HUMAN
27	63	52.5	1247	1	JAG2_MOUSE
28	62	51.7	29	1	CKX7_CONCT
29	62	51.7	73	1	DLI1_RAT
30	62	51.7	714	1	DLI1_MOUSE
31	62	51.7	722	1	DLI1_MOUSE
32	62	51.7	723	1	FBP1_STRPU
33	62	51.7	1064	1	FBP1_STRPU

34	61.5	51.2	36	1	TXM1_AGEAP	P11057 agelenopsis
35	61	50.8	29	1	CKOD_CONMA	Q26350 conus magus
36	61	50.8	1408	1	SERR_DROME	P18168 drosophila
37	61	50.8	1480	1	SLIT_DROME	P24014 drosophila
38	60	50.0	833	1	DL_DROME	P10041 drosophila
39	60	50.0	1295	1	GLP1_CAEEL	P13508 caenorhabdit
40	60	50.0	1376	1	CRBH_HUMAN	P82279 homo sapien
41	59	49.2	25	1	CKOB_CONMA	P05485 conus magus
42	59	49.2	43	1	MTA_COLVI	P27086 colinus vir
43	59	49.2	53	1	CTL1_NPYOP	O10367 oryza pseu
44	59	49.2	53	1	CTL1_NPYOP	P41416 autographa
45	59	49.2	63	1	MT_CHICK	P09576 gallus gall

ALIGNMENTS

RESULT 1
ID CKX7_CONPU STANDARD: PRT: 72 AA.
AC P56633;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Kappa-conotoxin PVIIA precursor (Fin-popping peptide).
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RN SEQUENCE FROM N.A., AND SYNTHESIS.
RX MEDLINE=98079023; PubMed=9417043;
RA Shon K.-J., Stocker M., Terlau H., Stuehmer W., Jacobsen R.B.,
RA Walker C.S., Grille M.M., Watkins M., Hillyard D.R., Gray W.R.,
RA Olivera B.M.;
RT "Kappa-conotoxin PVIIA is a peptide inhibiting the shaker K+
RT channel.";
RL J. Biol. Chem. 273:33-38(1998).
RN [2]
RN SEQUENCE OF 46-72, AND SYNTHESIS.
RX PubMed=12074021;
RA Terlau H., Shon K.-J., Grille M.M., Stocker M., Stuehmer W.,
RA Olivera B.M.;
RT "Strategy for rapid immobilization of prey by a flash-hunting marine
RT snail.";
RL Nature 381:148-151(1996).
RN [3]
RN STRUCTURE BY NMR.
RX TISSUE=Venom;
RX MEDLINE=98104087; PubMed=9438859;
RA Scanlon M.J., Naranjo D., Thomas L., Alewood P.F., Lewis R.J.,
RA Craik D.J.;
RT "Solution structure and proposed binding mechanism of a novel
RT potassium channel toxin kappa-conotoxin PVIIA.";
RL Structure 5:1585-1597(1997).
RN [4]
RN STRUCTURE BY NMR.
RX MEDLINE=98217293; PubMed=9548922;
RA Savarin P., Guennegues M., Gilquin B., Lamthanh H., Gasparini S.,
RA Zlin-Justin S., Menez A.;
RT "Three-dimensional structure of kappa-conotoxin PVIIA, a novel
RT potassium channel-blocking toxin from cone snails.";
RL Biochemistry 37:5407-5416(1998).
RN [5]
RN MUTAGENESIS OF ARG-47, ILE-48, PRO-49, ASN-50, GLN-51, LYS-52, PHE-54;
RX PHE-54; GLN-55; HIS-56; LEU-57; ASP-58; ASP-59; SER-62; ARG-63;
RP LYS-64; ARG-67; PHE-68; ASN-69 AND LYS-70.
RX PubMed=10818087;
RA Jacobsen R.B., Koch E.D., Lange-Majack B., Stocker M., Verhey J.,
RA Van Wagoner R.M., Vyazovkina A., Olivera B.M., Terlau H.;
RT "Single amino acid substitutions in kappa-conotoxin PVIIA disrupt
RT interaction with the shaker K+ channel.";
RL J. Biol. Chem. 275:24639-24644(2000).

FT DISULFID 53 65
 FT DISULFID 60 71 AMIDATION (G-72 PROVIDE AMIDE GROUP).
 FT MOD_RES 71 71
 SQ SEQUENCE 72 AA; 7741 MW; 1F73546AD39908 CRC64;
 Query Match 64.2%; Score 77; DB 1; Length 72;
 Best Local Similarity 34.6%; Pred. No. 0.12;
 Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CXINQXQXQXLDCCSXNXXNXC 26
 1:::1:::1:::1:::1
 Db 46 CKIKGSCSKRTSYDCSCSGCRSGKC 71
 RESULT 3
 CXQC CONCT STANDARD; PRT; 26 AA.
 AC P58919;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Omega-conotoxin CVIC.
 OS Conus calus (Cat cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conidae; Conus.
 OX NCBI_Taxid-101291;
 RN (1)
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Venom;
 RX PubMed-10938268;
 RA Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A.,
 RA Shape I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,
 RA Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.;
 RT "Novel omega-conotoxins from Conus calus discriminate among neuronal
 calcium channel subtypes.";
 RT J. Biol. Chem. 275:35335-35344(2000).
 RL J. Biol. Chem. 275:35335-35344(2000).
 CC -1- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 and block voltage-sensitive calcium channels (VSCC) (By
 similarity). This toxin blocks N-, P-, and Q-type calcium
 channels.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
 FAMILY.
 KW Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
 KW Amidation.
 FT DISULFID 1 16 BY SIMILARITY.
 FT DISULFID 8 20 BY SIMILARITY.
 FT DISULFID 15 26 BY SIMILARITY.
 FT MOD_RES 26 26 AMIDATION.
 SQ SEQUENCE 26 AA; 2790 MW; 56EFC82335C4A8B CRC64;
 Query Match 60.8%; Score 73; DB 1; Length 26;
 Best Local Similarity 30.8%; Pred. No. 0.13;
 Matches 8; Conservative 14; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CXINQXQXQXLDCCSXNXXNXC 26
 1:::1:::1:::1:::1
 Db 1 CKRGQSCSKLMYDCSCSGCRSGKC 26
 RESULT 4
 NOTC_XENLA STANDARD; PRT; 2524 AA.
 AC P21783;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neurogenic locus notch protein homolog precursor (XOTCH protein).
 GN XOTCH.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;

OC Xenopodinae; Xenopus.
 OX NCBI_Taxid-8355;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90385285; PubMed=2402639;
 RA Cofman C., Harris W., Kintner C.;
 RT "Xotch, the Xenopus homolog of Drosophila notch.";
 RT Science 249:1438-1441(1990).
 RN (2)
 RP REVISIONS TO 1759-1782.
 RA Kintner C.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED ALMOST UNIFORMLY IN EARLY EMBRYOS.
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
 CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
 CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M33874; AB02039.1; -
 DR PIR: A35844; A35844.
 DR HSSP: P00740; 1EDM.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF-2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF-IT.
 DR InterPro: IPR000800; Notch.
 DR Pfam: PF00008; EGF; 36.
 DR Pfam: PF00023; ank; 6.
 DR Pfam: PF00066; notch; 3.
 DR PRINTS: PR00010; EGFRLD.
 DR PRINTS: PR01452; NOTCH.
 DR SMART: SM00248; ANK; 5.
 DR SMART: SM00179; EGF_CA; 23.
 DR SMART: SM00001; EGF-like; 11.
 DR SMART: SM00004; NL; 2.
 DR PROSITE: PS50088; ANK_REPEAT; 4.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 23.
 DR PROSITE: PS00022; EGF_1; 34.
 DR PROSITE: PS01186; EGF_2; 29.
 DR PROSITE: PS01187; EGF_CA; 21.
 KW Differentiation; Neurogenesis; Repeat; ANK repeat; EGF-like domain;
 KW Transmembrane; Signal; Glycoprotein.
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 FT CHAIN 20 2524
 FT DOMAIN 20 1728
 FT TRANSMEM 1729 1750
 FT DOMAIN 1751 2524
 FT DOMAIN 20 57
 FT DOMAIN 58 99
 FT DOMAIN 102 140
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 FT DOMAIN 179 215
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 FT DOMAIN 294 332
 FT DOMAIN 334 370
 FT DOMAIN 371 409
 FT DOMAIN 411 449
 FT DOMAIN 451 487
 FT DOMAIN 489 525
 FT DOMAIN 527 563
 FT POTENTIAL.
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 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT EGF-LIKE 1.
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 FT EGF-LIKE 3.
 FT EGF-LIKE 4.
 FT EGF-LIKE 5.
 FT EGF-LIKE 6.
 FT EGF-LIKE 7.
 FT EGF-LIKE 8.
 FT EGF-LIKE 9.
 FT EGF-LIKE 10.
 FT EGF-LIKE 11.
 FT EGF-LIKE 12.
 FT EGF-LIKE 13.
 FT EGF-LIKE 14.

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FT DOMAIN 565 600 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 602 638 EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 640 673 EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 677 713 EGF-LIKE 18, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 715 750 EGF-LIKE 19, CALCIUM-BINDING (POTENTIAL).
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FT DOMAIN 868 904 EGF-LIKE 23, CALCIUM-BINDING (POTENTIAL).
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FT DOMAIN 1306 1346 EGF-LIKE 34, CALCIUM-BINDING (POTENTIAL).
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FT DOMAIN 1386 1424 EGF-LIKE 36, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1441 1478 EGF-LIKE 37, CALCIUM-BINDING (POTENTIAL).
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FT REPEAT 1521 1560 LIN/NOTCH 2.
FT REPEAT 1561 1600 LIN/NOTCH 3.
FT REPEAT 1601 1640 ANK 1.
FT REPEAT 1641 1680 ANK 2.
FT REPEAT 1681 1720 ANK 3.
FT REPEAT 1721 1760 ANK 4.
FT REPEAT 1761 1800 ANK 5.
FT REPEAT 1801 1840 ANK 6.
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Query Match 60.0%; Score 72; DB 1; Length 2524;
Best local Similarity 34.6%; Pred. No. 6.5;
Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

OY 2 XIXNOCXQXMDCCSXCMXKXCV 27
DB 247 GFSGONCEHIDPCPSNCRNGTCV 272

RESULT 5
CXOC CONMA STANDARD; PRT; 29 AA.
ID CXOC CONMA
AC P37300;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Omega-conotoxin MV1c precursor (SNX-230) (Fragment).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_Taxid=6492;
RN [1]
RP SEQUENCE FROM N.A., AND SYNTHESIS.
RX MEDLINE=92337922; PubMed=1352986;
RA Hillyard D.R., Monte V.D., Mintz I.M., Bean B.P., Nadasdi L.,
RA Ramachandran J., Miltanich G.P., Azimi-Zoonooz A., McIntosh J.M.,
RA Cruz L.J., Imperial J.S., Olivera B.M.,
RA "A new Conus peptide ligand for mammalian presynaptic Ca2+ channels."
RT

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DR EMBL: AF308602; AAC33848.1; -
 DR EMBL: M73980; AAA60614.1; -
 DR HSSP: P00740; IEDM.
 DR Genew: HGNC:7881; NOTCH1.
 DR MIM: 190198; -
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_11.
 DR Pfam: PF00080; Notch.
 DR Pfam: PF00008; EGF; 36.
 DR Pfam: PF00023; ank; 6.
 DR Pfam: PF00066; notch; 3.
 DR SMART: SM00248; ANK; 5.
 DR SMART: SM00179; EGF_Ca; 22.
 DR SMART: SM00001; EGF_like; 13.
 DR PROSITE: PS50088; ANK_REPEAT; 4.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 20.
 DR PROSITE: PS00022; EGF_1; 34.
 DR PROSITE: PS01186; EGF_2; 26.
 DR PROSITE: PS01187; EGF_Ca; 18.
 DR Receptor: Transcription regulation; Activator; Differentiation;
 KW Developmental protein; Repeat; ANK repeat; EGF-like domain;
 KW Transmembrane; Glycoprotein; Signal; Phosphorylation.
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OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-Oregon-R; TISSUE-Embryo;
 RX MEDLINE=90263104; PubMed=2344615;
 RA Tepass U., Theres C., Knust E.;
 RT "Crumbs encodes an EGF-like protein expressed on apical membranes of
 RT Drosophila epithelial cells and required for organization of
 RT epithelia.";
 RL Cell 61:787-799(1990).
 RN (2)
 RP SEQUENCE OF 1663-1955 FROM N.A.
 RC TISSUE-Embryo;
 RX MEDLINE=87218537; PubMed=3107986;
 RA Knust E., Dietrich U., Tepass U., Bremer K.A., Weigelt D.,
 RA Vaessin H., Campos-Ortega J.A.;
 RT "EGF homologous sequences encoded in the genome of Drosophila
 RT melanogaster, and their relation to neurogenic genes.";
 RL EMO J. 6:761-766(1987).
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE DEVELOPMENT OF EPITHELIA,
 CC POSSIBLY FOR THE ESTABLISHMENT AND/OR MAINTENANCE OF CELL
 CC POLARITY. IT MAY ACT AS A SIGNAL.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- PTM: PHOSPHORYLATED IN THE CYTOPLASMIC DOMAIN (POTENTIAL).
 CC -1- SIMILARITY: CONTAINS 29 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: M33753; AAA28428.1; ALT-SEQ.
 DR EMBL: X05144; CAA28793.1; -
 DR PIR: B26637; B26637.
 DR PIR: A35672; A35672.
 DR HSP: P00740; IEDM.
 DR FLYBase: FBgn0000368; crb.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_II.
 DR InterPro: IPR001791; Laminin_G.
 DR Pfam: PF00008; EGF_26.
 DR Pfam: PF00054; laminin_G_3.
 DR PRINTS: PR00010; EGFRIOD.
 DR SMART: SM00179; EGF_CA_11.
 DR SMART: SM00001; EGF_Like_16.
 DR SMART: SM00282; Lamg_3.
 DR PROSITE: PS00010; ASX_HYDROXYL; 15.
 DR PROSITE: PS00022; EGF_1; 26.
 DR PROSITE: PS01186; EGF_2; 17.
 DR PROSITE: PS01187; EGF_CA; 12.
 DR PROSITE: PS50025; LAM_G_DOMAIN; 3.
 DR Differentiation: Repeat; EGF-like domain; Transmembrane;
 KW Glycoprotein; Signal; Phosphorylation.
 FT SIGNAL 1 90
 FT CHAIN 91 2139 CRUMBS PROTEIN.
 FT DOMAIN 91 2084 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 2085 2111 POTENTIAL.
 FT DOMAIN 2112 2139 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 267 303 EGF-LIKE 1.
 FT DOMAIN 306 343 EGF-LIKE 2.
 FT DOMAIN 348 386 EGF-LIKE 3.
 FT DOMAIN 388 425 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN

FT DOMAIN 427 463 EGF-LIKE 5.
 FT DOMAIN 464 500 EGF-LIKE 6.
 FT DOMAIN 501 532 EGF-LIKE 7.
 FT DOMAIN 545 581 EGF-LIKE 8.
 FT DOMAIN 582 611 EGF-LIKE 9.
 FT DOMAIN 609 646 EGF-LIKE 10.
 FT DOMAIN 648 685 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 687 723 EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 725 761 EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 763 800 EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 802 838 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 840 902 EGF-LIKE 16.
 FT DOMAIN 904 940 EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 942 978 EGF-LIKE 18, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 980 1021 EGF-LIKE 19.
 FT DOMAIN 1023 1205 LAMININ G-LIKE 1.
 FT DOMAIN 1207 1243 EGF-LIKE 20.
 FT DOMAIN 1250 1480 LAMININ G-LIKE 2.
 FT DOMAIN 1481 1517 EGF-LIKE 21.
 FT DOMAIN 1558 1758 LAMININ G-LIKE 3.
 FT DOMAIN 1759 1795 EGF-LIKE 22.
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 FT DOMAIN 1874 1915 EGF-LIKE 25.
 FT DOMAIN 1915 1951 EGF-LIKE 26.
 FT DOMAIN 1953 1989 EGF-LIKE 27, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1991 2029 EGF-LIKE 28, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 2030 2070 EGF-LIKE 29.
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FT CARBOHYD 37 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 198 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 550 550 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 55.8% Score 67; DB 1; Length 2139;
Best Local Similarity 28.0%; Pred. No. 18;
Matches 7; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

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RC TISSUE=Embryo; PubMed=8297791;
RX MEDLINE=94128602;
RA Bierkamp C., Campos-Ortega J.A.;
RT "A zebrafish homologue of the Drosophila neurogenic gene Notch and
its pattern of transcription during early embryogenesis.";
RL Mech. Dev. 43:87-100(1993).
CC -1- FUNCTION: IMPLICATED IN CELL FATE SPECIFICATIONS DURING
CC EMBRYO DEVELOPMENT. MAY BE INVOLVED IN THE FORMATION OF THE
CC NEURAL PLATE, NOTOCHORD AND BRAIN VESICLES.
CC SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DEVELOPMENTAL STAGE: Expressed in all cells in pregastrulation
CC stages. During gastrulation is differentially expressed,
CC accumulating predominantly in the prechordal mesoderm and
CC notochord. At the end of gastrulation, expressed along the
CC anterior-posterior axis including the developing neural plate
CC and differentiating mesoderm. Also present in the developing
CC brain and head regions.
CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
CC -----
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DR HSPB; P00740; IEDM.
DR ZFIN; ZDB-GENE-990415-173; notchia.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF_Like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_IL.
DR InterPro: IPR000800; Notch.
DR Pfam: PF00008; EGF; 36.
DR Pfam: PF00023; ank; 6.
DR Pfam: PF00066; notch; 3.
DR PRINTS; PR00010; EGFBLDOD.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00248; ANK; 5.
DR SMART; SM00179; EGF_CA; 19.
DR SMART; SM00001; EGF_Like; 16.
DR PROSITE; PS00004; NL; 3.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 23.
DR PROSITE; PS00022; EGF_1; 34.
DR PROSITE; PS01186; EGF_2; 28.
DR PROSITE; PS01187; EGF_CA; 22.
KW Receptor; Transcription regulation; Activator; Differentiation;
KW developmental protein; Neurogenesis; Repeat; ANK repeat;
KW EGF-like domain; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 2437
FT DOMAIN 21 1724 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1725 1747
FT DOMAIN 1748 2437 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 21 57 EGF-LIKE 1.
FT DOMAIN 58 98 EGF-LIKE 2.
FT DOMAIN 101 138 EGF-LIKE 3.
FT DOMAIN 139 175 EGF-LIKE 4.
FT DOMAIN 176 215 EGF-LIKE 5.
FT DOMAIN 217 254 EGF-LIKE 6.
FT DOMAIN 256 292 EGF-LIKE 7.
FT DOMAIN 294 332 EGF-LIKE 8.
FT DOMAIN 334 370 EGF-LIKE 9.
FT DOMAIN 371 409 EGF-LIKE 10.

```


[2] SEQUENCE OF 731-1899 FROM N.A. (ISOFORM 2), AND DEVELOPMENTAL STAGE.
 RP STRAIN-CD-1: TISSUE-Embryo;
 RC MEDLINE-93050801: PubMed-1426644;
 RX Reaume A.G., Conlon R.A., Ziringibl R., Yamaguchi T.P., Rossant J.;
 RA "Expression analysis of a Notch homologue in the mouse embryo.";
 RT Dev. Biol. 154:377-387(1992).
 RL [3]
 RN SEQUENCE OF 1551-1647 FROM N.A. (ISOFORM 1), AND DEVELOPMENTAL STAGE.
 RP TISSUE-Embryo;
 RC MEDLINE-93048835: PubMed-1425352;
 RX Franco del Amo F., Smith D.E., Swiatek P.J., Gendron-Maguire M.,
 RA Greenspan R.J., McMahon A.P., Gridley T.;
 RT "Expression pattern of Notch, a mouse homolog of Drosophila Notch,
 RT suggests an important role in early postimplantation mouse
 RT development.";
 RL Development 115:737-744(1992).
 RN [4]
 RN SEQUENCE OF 1161-1547 FROM N.A.
 RP STRAIN-C57BL/6 X CBA; TISSUE-Embryo;
 RX MEDLINE-93178563: PubMed-8440332;
 RA Lardelli M., Lendahl U.;
 RT "Notch A and Notch B-two mouse Notch homologues coexpressed in a
 RT wide variety of tissues.";
 RL Exp. Cell Res. 204:364-372(1993).
 RN [5]
 RN SEQUENCE OF 1659-1673 FROM N.A.
 RP MEDLINE-99364499: PubMed-10437788;
 RX Lee J.S., Ishimoto A., Yanagawa S.I.;
 RA "Murine leukemia provirus-mediated activation of the Notch1 gene leads
 RT to induction of HES-1 in a mouse T lymphoma cell line, DL-3.";
 RL FEBS Lett. 455:276-280(1999).
 RN [6]
 RN SEQUENCE OF 1950-2201 FROM N.A.
 RP MEDLINE-98029496: PubMed-9384671;
 RX Messerle M., Folio M., Nehls M., Eggert H., Boehm T.;
 RA "Dynamic changes in gene expression during in vitro differentiation of
 RT mouse embryonic stem cells.";
 RL Cytokines Cell. Mol. Ther. 1:139-143(1995).
 RN [7]
 RN SEQUENCE OF 1655-1659, CLEAVAGE BY FURIN-LIKE CONVERTASE, AND
 RP MUTAGENESIS OF 1651-ARG-GLN-ARG-ARG-1654.
 RX MEDLINE-98318619: PubMed-9653148;
 RA Logeat F., Bessia C., Bron C., Lebail O., Jarrault S., Seidah N.G.,
 RA Israel A.;
 RT "The Notch1 receptor is cleaved constitutively by a furin-like
 RT convertase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8108-8112(1998).
 RN [8]
 RN PARTIAL SEQUENCE, AND POST-TRANSLATIONAL PROCESSING.
 RP MEDLINE-21533956: PubMed-11518718;
 RX Saxena M.T., Schroeter E.H., Munni J.S., Kopan R.;
 RA "Murine notch homologs (N1-4) undergo presenilin-dependent
 RT proteolysis.";
 RL J. Biol. Chem. 276:40268-40273(2001).
 RN [9]
 RN POST-TRANSLATIONAL PROCESSING.
 RP MEDLINE-21374376: PubMed-1145941;
 RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
 RT "Conservation of the biochemical mechanisms of signal transduction
 RT among mammalian Notch family members.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
 CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands
 CC Jagged1, Jagged2 and Delta1 to regulate cell-fate determination.
 CC Upon ligand activation through the released notch intracellular
 CC domain (NICD) it forms a transcriptional activator complex with
 CC RBP-J kappa and activates genes of the enhancer of split locus.
 CC Affects the implementation of differentiation, proliferation and
 CC apoptotic programs (By similarity). May play an essential role in
 CC postimplantation development, probably in some aspect of cell
 CC specification and/or differentiation. May be involved in mesoderm
 CC development, somit formation and neurogenesis. Involved in the
 CC maturation of both CD4+ and CD8+ cells in the thymus.

-1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds.
 CC
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following
 CC proteolytical processing NICD is translocated to the nucleus.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Highly expressed in the brain, lung and
 CC thymus. Expressed at lower levels in the spleen, bone-marrow,
 CC spinal cord, eyes, mammary gland, liver, intestine, skeletal
 CC muscle, kidney and heart.
 CC -1- DEVELOPMENTAL STAGE: First detected in the mesoderm at 7.5 d.p.c.
 CC By 8.5 d.p.c. highly expressed in presomitic mesoderm, mesenchyme
 CC and endothelial cells, while much lower levels are seen in the
 CC neuroepithelium. Between 9.5-10.5 d.p.c. expressed at high levels
 CC in the neuroepithelium. At 13.5 d.p.c. expressed in the surface
 CC ectoderm, eye and developing whisker follicles.
 CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form
 CC which is proteolytically cleaved by a furin-like convertase in the
 CC trans-golgi network before it reaches the plasma membrane to yield
 CC an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme
 CC (TACE) to yield a membrane-associated intermediate fragment called
 CC notch extracellular truncation (NEXT). This fragment is then
 CC cleaved by presenilin dependent gamma-secretase to release a
 CC notch-derived peptide containing the intracellular domain (NICD)
 CC from the membrane.
 CC -1- PTM: Phosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
 CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
 CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.
 CC
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: 211886; CAA77941.1; -
 CC EMBL: L02613; AAK14898.1; -
 CC EMBL: X68278; CAA48339.1; -
 CC EMBL: AJ238029; CAA40733.1; -
 CC EMBL: X82562; CAA57909.1; -
 CC HSSP: P00740; 1EDM.
 CC MGD: MGI:97363; Notch1.
 CC InterPro: IPR002110; ANK.
 CC InterPro: IPR000152; Asx_hydroxyl.
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR000742; EGF_2.
 CC InterPro: IPR001881; EGF_CA.
 CC InterPro: IPR001438; EGF_II.
 CC InterPro: IPR000800; Notch.
 CC Pfam: PF00008; EGF_35.
 CC Pfam: PF00023; ank; 7.
 CC Pfam: PF00066; notch; 3.
 CC PRINTS: PR00010; EGFLOOD.
 CC PRINTS: PR01452; NOTCH.
 CC SMART: SM00248; ANK; 3.
 CC SMART: SM00179; EGF_CA; 23.
 CC SMART: SM00001; EGF-like; 11.
 CC SMART: SM00004; NL; 2.
 CC PROSITE: PS50068; ANK_REPEAT; 2.
 CC PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 CC PROSITE: PS00010; ASX_HYDROXYL; 22.
 CC PROSITE: PS00022; EGF_1; 34.
 CC PROSITE: PS01186; EGF_2; 27.
 CC PROSITE: PS01187; EGF_CA; 21.
 CC Receptor; Transcription regulation; Activator; Differentiation;
 CC Developmental protein; Repeat; ANK repeat; EGF-like domain;
 CC

DR InterPro: IPR002049; Laminin_EGF.
 DR InterPro: IPR000800; Notch.
 DR Pfam: PF00008; EGF_36.
 DR Pfam: PF00023; ank; 6.
 DR Pfam: PF00066; notch; 3.
 DR PRINTS: PR00010; EGFBLD.
 DR PRINTS: PR00011; EGFAMININ.
 DR PRINTS: PR01452; NOTCH.
 DR SMART: SM00248; ANK; 5.
 DR SMART: SM00179; EGF_CA; 25.
 DR SMART: SM00001; EGF_Like; 10.
 DR SMART: SM00004; NL; 2.
 DR PROSITE: PSS0088; ANK_REPEAT; 4.
 DR PROSITE: PSS0297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PSS0010; ASX_HYDROXYL; 22.
 DR PROSITE: PSS0022; EGF_1; 35.
 DR PROSITE: PSS0186; EGF_2; 26.
 DR PROSITE: PSS0187; EGF_CA; 21.
 KW Receptor; Transcription regulation; Activator; Differentiation;
 KW Developmental protein; Repeat; ANK repeat; EGF-like domain;
 KW Transmembrane; Glycoprotein; Signal; Phosphorylation.
 FT CHAIN 1 18
 FT CHAIN 19 2531
 FT CHAIN 1711 2531
 FT CHAIN 1744 2531
 FT DOMAIN 19 1723
 FT TRANSMEM 1724 1746
 FT DOMAIN 1747 2531
 FT DOMAIN 20 58
 FT DOMAIN 59 99
 FT DOMAIN 102 139
 FT DOMAIN 140 176
 FT DOMAIN 178 216
 FT DOMAIN 218 253
 FT DOMAIN 257 293
 FT DOMAIN 295 333
 FT DOMAIN 335 371
 FT DOMAIN 372 410
 FT DOMAIN 412 450
 FT DOMAIN 452 488
 FT DOMAIN 490 526
 FT DOMAIN 528 564
 FT DOMAIN 566 601
 FT DOMAIN 603 639
 FT DOMAIN 641 676
 FT DOMAIN 678 714
 FT DOMAIN 716 751
 FT DOMAIN 753 789
 FT DOMAIN 791 827
 FT DOMAIN 829 869
 FT DOMAIN 869 905
 FT DOMAIN 907 943
 FT DOMAIN 945 981
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 FT DOMAIN 1021 1057
 FT DOMAIN 1059 1095
 FT DOMAIN 1097 1143
 FT DOMAIN 1145 1181
 FT DOMAIN 1183 1219
 FT DOMAIN 1221 1265
 FT DOMAIN 1267 1305
 FT DOMAIN 1307 1346
 FT DOMAIN 1348 1384
 FT DOMAIN 1387 1426
 FT DOMAIN 1441 1480
 FT REPEAT 1481 1522
 FT REPEAT 1523 1562
 FT REPEAT 1917 1946
 FT REPEAT 1950 1980
 FT REPEAT 1984 2013
 FT REPEAT 2017 2046

FT REPEAT 2050 2079 ANK 5.
 FT DOMAIN 1730 1733 POLY-ALA.
 FT DOMAIN 1891 1894 POLY-GLU.
 FT DOMAIN 2258 2261 POLY-PRO.
 FT DOMAIN 2497 2500 POLY-SER.
 FT SITE 1654 1655 CLEAVAGE BY FURIN-LIKE PROTEASE (BY SIMILARITY).
 FT DISULFID 24 37 BY SIMILARITY.
 FT DISULFID 31 46 BY SIMILARITY.
 FT DISULFID 48 57 BY SIMILARITY.
 FT DISULFID 63 74 BY SIMILARITY.
 FT DISULFID 68 87 BY SIMILARITY.
 FT DISULFID 89 98 BY SIMILARITY.
 FT DISULFID 106 117 BY SIMILARITY.
 FT DISULFID 111 127 BY SIMILARITY.
 FT DISULFID 129 138 BY SIMILARITY.
 FT DISULFID 144 153 BY SIMILARITY.
 FT DISULFID 149 164 BY SIMILARITY.
 FT DISULFID 166 175 BY SIMILARITY.
 FT DISULFID 182 195 BY SIMILARITY.
 FT DISULFID 189 204 BY SIMILARITY.
 FT DISULFID 206 215 BY SIMILARITY.
 FT DISULFID 222 233 BY SIMILARITY.
 FT DISULFID 227 243 BY SIMILARITY.
 FT DISULFID 245 254 BY SIMILARITY.
 FT DISULFID 261 272 BY SIMILARITY.

Query Match 55.88; Score 67; DB 1; Length 2531;
 Best local Similarity 30.88; Pred. No. 20;
 Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
 Oy 2 XIXNXXCXQXLDCCSXKXNXXCV 27
 DB 248 GPAGNCCENVDPCGNNCKNGACV 273

RESULT 11
 NTC2_MOUSE STANDARD; PRT; 2470 AA.
 AC 035516; 060941; 006008;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neurogenic locus notch homolog protein 2 precursor (Notch 2) (Motch B).
 GN NOTCH2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Thymus;
 RA Hanada Y., Higuchi M., Tsujimoto Y.;
 RT "Complete amino acid sequence and multiple sequence alignment of a single copy of mouse Notch2 gene."
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 316-1518 FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Embryo;
 RX MEDLINE=93178563; PubMed=8440332;
 RA Lardelli M., Lendahl U.;
 RT "Motch A and Motch B-two mouse Notch homologues coexpressed in a wide variety of tissues."
 RL Exp. Cell Res. 204:364-372(1993).
 RN [3]
 RP SEQUENCE OF 1765-2153 FROM N.A.
 RX MEDLINE=97075110; PubMed=8917536;
 RA Milner L.A., Bigas A., Kopan R., Brashem-Stein C., Bernstein I.D., Martin D.I.;
 RT "Inhibition of granulocytic differentiation by mNotch1."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:13014-13019(1996).
 RN [4]

RP FUNCTION.
 RX MEDLINE=99396706; PubMed=10393120;
 RA Hamada Y., Kadokawa Y., Okabe M., Ikawa M., Coleman J.R.,
 RA Tsujimoto Y.;
 RT "Mutation in ankyrin repeats of the mouse Notch2 gene induces early
 RT embryonic lethality.";
 RL Development 126:3415-3424(1999).
 RN [5]
 RP DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING.
 RX MEDLINE=9533893; PubMed=7609614;
 RA Higuchi M., Kiyama H., Hayakawa T., Hamada Y., Tsujimoto Y.;
 RT "Differential expression of Notch1 and Notch2 in developing and adult
 RT mouse brain.";
 RL Brain Res. Mol. Brain Res. 29:263-272(1995).
 RN [6]
 RP POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.
 RX MEDLINE=21523956; PubMed=11518718;
 RA Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
 RT "Murine notch homologs (N1-4) undergo presenilin-dependent
 RT proteolysis.";
 RL J. Biol. Chem. 276:40268-40273(2001).
 RN [7]
 RP POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.
 RX MEDLINE=21374376; PubMed=11459941;
 RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
 RT "Conservation of the biochemical mechanisms of signal transduction
 RT among mammalian Notch family members.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
 CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands
 CC Jagged1, Jagged2 and Delta1 to regulate cell-fate determination.
 CC Upon ligand activation through the released notch intracellular
 CC domain (NICD) it forms a transcriptional activator complex with
 CC RBP-J kappa and activates genes of the enhancer of split locus.
 CC Affects the implementation of differentiation, proliferation and
 CC apoptotic programs (by similarity). May play an essential role in
 CC postimplantation development, probably in some aspect of cell
 CC specification and/or differentiation.
 CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
 CC terminal fragment N(EC) which are probably linked by disulfide
 CC bonds.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following
 CC proteolytical processing NICD is translocated to the nucleus.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Expressed in the brain, liver, kidney,
 CC neuroepithelia, somites, optic vesicles and branchial arches, but
 CC not heart.
 CC -1- DEVELOPMENTAL STAGE: Expressed in the embryonic ventricular zone,
 CC the postnatal endodermal cells, and the choroid plexus throughout
 CC embryonic and postnatal development.
 CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form
 CC which is proteolytically cleaved by a furin-like convertase in the
 CC trans-Golgi network before it reaches the plasma membrane to yield
 CC an active, ligand-accessible form. Cleavage results in a C-
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme
 CC (TACE) to yield a membrane-associated intermediate fragment called
 CC notch extracellular truncation (NEXT). This fragment is then
 CC cleaved by presenilin dependent gamma-secretase to release a
 CC notch-derived peptide containing the intracellular domain (NICD)
 CC from the membrane.
 CC -1- PTM: Phosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
 CC -1- SIMILARITY: CONTAINS 34.5 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 LIN/NOTCH REPEATS.
 CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
 CC -----
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 CC -----
 CC EMBL: D32210; BAA22094.1; -
 CC EMBL: X68279; CAA48340.1; -
 CC EMBL: U31861; AAC52924.1; -
 CC HSSP: P16109; IFSB.
 CC MGD: MGI:97364; Notch2.
 CC InterPro: IPR002110; ANK.
 CC InterPro: IPR000152; Asx_hydroxyl.
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR000742; EGF_2.
 CC InterPro: IPR001861; EGF_CA.
 CC InterPro: IPR001438; EGF_II.
 CC InterPro: IPR000800; Notch.
 CC Pfam: PF00008; EGF_35.
 CC Pfam: PF00023; ank; 6.
 CC Pfam: PF00066; notch; 2.
 CC PRINTS: PR00010; EGFBL00D.
 CC PRINTS: PR01452; NOTCH.
 CC SMART: SM00248; ANK; 4.
 CC SMART: SM00179; EGF_CA; 22.
 CC SMART: SM00001; EGF_Like; 12.
 CC SMART: SM00004; NT; 3.
 CC PROSITE: PS50088; ANK_REPEAT; 4.
 CC PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 CC PROSITE: PS00010; ASX_HYDROXYL; 22.
 CC PROSITE: PS00022; EGF_1; 33.
 CC PROSITE: PS01186; EGF_2; 27.
 CC PROSITE: PS01187; EGF_CA; 22.
 CC Receptor; Transcription regulation; Activator; Differentiation;
 CC developmental protein; Repeat; ANK repeat; EGF-like domain;
 CC Transmembrane; Glycoprotein; Signal; Phosphorylation;
 CC Alternative splicing.
 CC FT SIGNAL 1 25
 CC FT CHAIN 26 2470
 CC FT CHAIN 1666 2470
 CC FT CHAIN 1667 2470
 CC FT CHAIN 26 1677
 CC FT TRANSMEM 1678 1698
 CC FT DOMAIN 1699 2470
 CC FT DOMAIN 26 63
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 CC FT DOMAIN 221 256
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 CC FT DOMAIN 568 603
 CC FT DOMAIN 605 641
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 CC FT DOMAIN 793 829
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 CC FT DOMAIN 1223 1260
 CC FT DOMAIN 1262 1300
 CC -----
 CC POTENTIAL.
 CC NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 2.
 CC NOTCH EXTRACELLULAR TRUNCATION.
 CC NOTCH INTRACELLULAR DOMAIN.
 CC EXTRACELLULAR (POTENTIAL).
 CC POTENTIAL.
 CC CYTOPLASMIC (POTENTIAL).
 CC EGF-LIKE 1.
 CC EGF-LIKE 2.
 CC EGF-LIKE 3.
 CC EGF-LIKE 4.
 CC EGF-LIKE 5.
 CC EGF-LIKE 6 (INCOMPLETE).
 CC EGF-LIKE 7.
 CC EGF-LIKE 8.
 CC EGF-LIKE 9.
 CC EGF-LIKE 10.
 CC EGF-LIKE 11.
 CC EGF-LIKE 12.
 CC EGF-LIKE 13.
 CC EGF-LIKE 14.
 CC EGF-LIKE 15.
 CC EGF-LIKE 16.
 CC EGF-LIKE 17.
 CC EGF-LIKE 18.
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 CC EGF-LIKE 24.
 CC EGF-LIKE 25.
 CC EGF-LIKE 26.
 CC EGF-LIKE 27.
 CC EGF-LIKE 28.
 CC EGF-LIKE 29.
 CC EGF-LIKE 30.
 CC EGF-LIKE 31.
 CC EGF-LIKE 32.
 CC EGF-LIKE 33.


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FT DOMAIN 1302 1345 EGF-LIKE 34.
FT DOMAIN 1372 1410 EGF-LIKE 35.
FT REPEAT 1418 1454 LTN/NOTCH 1.
FT REPEAT 1501 1533 LTN/NOTCH 2.
FT REPEAT 1825 1869 ANK 1.
FT REPEAT 1874 1903 ANK 2.
FT REPEAT 1907 1937 ANK 3.
FT REPEAT 1941 1970 ANK 4.
FT REPEAT 1974 2003 ANK 5.
FT REPEAT 2007 2036 ANK 6.
FT DOMAIN 1645 1648 POLY-ALA.
FT DOMAIN 1992 1995 POLY-LEU.
FT DOMAIN 2183 2189 POLY-ALA.
FT DOMAIN 2425 2428 POLY-SER.
FT DOMAIN 2445 2450 POLY-GLY.
FT DISULFID 28 41 BY SIMILARITY.
FT DISULFID 35 51 BY SIMILARITY.
FT DISULFID 53 62 BY SIMILARITY.
FT DISULFID 68 79 BY SIMILARITY.

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Query Match 55.0%; Score 66; DB 1; Length 2470;
Best Local Similarity 25.8%; Pred. NO. 25;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

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OY 1 CXIXN---OXQXQXLDCCSXKXNXXKCV 27
Db 322 CVCNMGSGDCSENIIDCAVASCOTPESTCI 352

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RESULT 12
NTC2_HUMAN STANDARD; PRT; 2471 AA.
AC 004721: O9H240: Q99734;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurogenic locus notch homolog protein 2 precursor (Notch 2) (hn2).
GN NOTCH2.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Blaumüller C.M., Mann R.S.;
RT "Human Notch2, a novel member of cell-fate determining NOTCH
RT family.",
RL submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Correa R.G., Camargo A.A., Moreira E.S., Simpson A.J.;
RT "Human Notch2, a novel member of cell-fate determining NOTCH
RT family.",
RL submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 967-1229 FROM N.A.
RC TISSUE=T-cell;
RA Lamason I., Devaux C., Mesnard J.M.;
RT "Partial sequence of EGF-like repeat domain of human Notch2 mRNA.",
RL submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1810-2447 FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=93265135; PubMed=1303260;
RA Stifant S., Blaumüller C.M., Redhead N.J., Hill R.E.,
RA Artavanis-Tsakonas S.;
RT "Human homologs of a Drosophila enhancer of split gene product define
RT a novel family of nuclear proteins.",
RL Nat. Genet. 2:119-127(1992).
RN [5]
RP POST-TRANSLATIONAL PROCESSING;
RX MEDLINE=97386453; PubMed=9244302;

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RA Blaumüller C.M., Qi H., Zagouras P., Artavanis-Tsakonas S.;
RT "Intracellular cleavage of Notch leads to a heterodimeric receptor on
RT the plasma membrane.",
RL Cell 90:281-291(1997).
RN [6]
RP IDENTIFICATION OF LIGANDS.
RX MEDLINE=99180765; PubMed=10079256;
RA Gray C.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
RT "Human ligands of the Notch receptor.",
RL Am. J. Pathol. 154:785-794(1999).
CC -i- FUNCTION: Functions as a receptor for membrane-bound ligands
CC Jagged1, Jagged2 and Delta1 to regulate cell-fate determination.
CC Upon ligand activation through the released notch intracellular
CC domain (NICD) it forms a transcriptional activator complex with
CC RBP-J kappa and activates genes of the enhancer of split locus.
CC Affects the implementation of differentiation, proliferation and
CC apoptotic programs (By similarity).
CC -i- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
CC terminal fragment N(EC) which are probably linked by disulfide
CC bonds (By similarity).
CC -i- SUBCELLULAR LOCATION: Type I membrane protein. Following
CC proteolytical processing NICD is translocated to the nucleus.
CC -i- TISSUE SPECIFICITY: Expressed in the brain, heart, kidney, lung,
CC skeletal muscle and liver.
CC -i- PTM: Synthesized in the endoplasmic reticulum as an inactive form
CC which is proteolytically cleaved by a furin-like convertase in the
CC trans-golgi network before it reaches the plasma membrane to yield
CC an active, ligand-accessible form. Cleavage results in a C-
CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following
CC ligand binding, it is cleaved by TNF-alpha converting enzyme
CC (TACE) to yield a membrane-associated intermediate fragment called
CC notch extracellular truncation (NEXT). This fragment is then
CC cleaved by presenilin dependent gamma-secretase to release a
CC notch-derived peptide containing the intracellular domain (NICD)
CC from the membrane (By similarity).
CC -i- PTM: Phosphorylated (By similarity).
CC -i- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
CC -i- SIMILARITY: CONTAINS 35 EGF-LIKE DOMAINS.
CC -i- SIMILARITY: CONTAINS 2 LTN/NOTCH REPEATS.
CC -i- SIMILARITY: CONTAINS 6 ANK REPEATS.
CC
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CC or send an email to license@sib-sib.ch).
CC
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CC EMBL; AF308601; AAA36377.2; -
CC EMBL; AF315356; AAG37073.1; -
CC EMBL; U77493; AAB19224.1; -
CC HSSP; P00740; IEDM.
CC Genew; HGNC:7882; NOTCH2.
CC MIM; 600275; -
CC InterPro; IPR002110; ANK.
CC InterPro; IPR000152; Asx_hydroxy1.
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR000742; EGF-2.
CC InterPro; IPR001881; EGF-Ca.
CC InterPro; IPR001438; EGF-IT.
CC InterPro; IPR002049; Laminin_EGF.
CC InterPro; IPR000800; Notch.
CC Pfam; PF00008; EGF; 35.
CC Pfam; PF00023; ank; 6.
CC Pfam; PF00066; notch; 2.
CC PRINTS; PR00010; EGFBLD.
CC PRINTS; PR00011; EGFAMININ.
CC SMART; SM00248; ANK; 4.
CC SMART; SM00179; EGF_CA; 22.
CC SMART; SM00001; EGF_like; 12.
CC SMART; SM00004; NL; 2.

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DR PROSITE: PS50088; ANK_REPEAT: 4.
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 DR PROSITE: PS00010; ASX_HYDROXYL: 22.
 DR PROSITE: PS00022; EGF_1; 34.
 DR PROSITE: PS01186; EGF_2; 29.
 DR PROSITE: PS01187; EGF_CA: 22.
 KW Receptor; Transcription regulation; Activator; Differentiation;
 KW Developmental protein; Repeat; ANK repeat; EGF-like domain;
 KW Transmembrane; Glycoprotein; Signal; Phosphorylation.
 FT SIGNAL 1 25
 FT CHAIN 26 2471
 FT CHAIN 1666 2471
 FT CHAIN 1697 2471
 FT DOMAIN 26 1677
 FT TRANSMEM 1678 1698
 FT DOMAIN 1699 2471
 FT DOMAIN 26 63
 FT DOMAIN 64 102
 FT DOMAIN 105 143
 FT DOMAIN 144 180
 FT DOMAIN 182 219
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 FT REPEAT 1876 1905
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 FT REPEAT 1943 1972
 FT REPEAT 1976 2005
 FT REPEAT 2009 2038
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 FT DISULFID 53 62
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 Best Local Similarity 25.8%; Pred. No. 25;
 Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;
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 DB 324 CVCVNGWSGDDCSNIDCAFASCTPGSTCI 354
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 AC Q9QW30;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neurogenic locus notch homolog protein 2 precursor (Notch 2).
 GN NOTCH2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=93202015; PubMed=1295745;
 RA Weinmaster G., Roberts V.J., Lemke G.;
 RT "Notch2: a second mammalian Notch gene.";
 RL Development 116:931-941(1992).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=21331789; PubMed=11438922;
 RA Irvay D.K., Zurcher S.D., Nguyen T., Weinmaster G.;
 RT "Expression patterns of Notch1, Notch2, and Notch3 suggest multiple functional roles for the Notch-Delta signaling system during brain development.";
 RL J. Comp. Neurol. 436:167-181(2001).
 CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Delta to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs. May play an essential role in postimplantation development, probably in some aspect of cell specification and/or differentiation (By similarity).
 CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.
 CC -1- TISSUE SPECIFICITY: Highly expressed in the spleen and choroid plexus in the brain. Expressed in postnatal central nervous system (CNS) germinal zones and, in early postnatal life, within numerous cells throughout the CNS. It is more highly localized to ventricular germinal zones. Also found in the heart, liver and kidney.
 CC -1- DEVELOPMENTAL STAGE: Expressed in the brain during E14 and E17.
 CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the

FT DISULFID 520 529 BY SIMILARITY.
 FT DISULFID 536 547 BY SIMILARITY.
 FT DISULFID 541 556 BY SIMILARITY.
 FT DISULFID 558 567 BY SIMILARITY.
 FT DISULFID 574 584 BY SIMILARITY.

Query Match 55.0%; Score 66; DB 1; Length 2471;
 Best Local Similarity 25.8%; Pred. No. 25;
 Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

QY 1 CRXN-----QXCKXUDDCCSXCKXNKNVCV 27
 Db 324 CVCVNGWSGDCCSENIIDCAFAFASCPGPTCI 354

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 AC P07207; P04154; 097458; 09W4T8;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neurogenic locus Notch protein precursor
 GN N OR EG:140611.1 OR EG:163A10.2 OR CG3936.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Oregon-R; TISSUE-Embryo;
 RX MEDLINE=86079539; PubMed=3935325;
 RA Wharton K.A., Johansen K.M., Xu T., Artavanis-Tsakonas S.;
 RT "Nucleotide sequence from the neurogenic locus notch implies a gene
 product that shares homology with proteins containing EGF-like
 repeats.";
 RT Cell 43:567-581(1985).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Canton-S; and Oregon-R; TISSUE-Embryo;
 RX MEDLINE=87064624; PubMed=3097517;
 RA Kidd S., Kelley M.R., Young M.W.;
 RT "Sequence of the notch locus of Drosophila melanogaster: relationship
 of the encoded protein to mammalian clotting and growth factors.";
 RT Mol. Cell. Biol. 6:3094-3108(1986).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale A., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostel R., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laske P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Mount D.R., Neison K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RT Science 287:2185-2195(2000).
 RL [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Oregon-R;
 RX MEDLINE=20196011; PubMed=10731137;
 RA Benos P.V., Galt M.K., Ashburner M., Murphy L., Harris D.,
 RA Barrett B.G., Ferraz C., Vidal S., Brun C., Demallies J., Cadieu E.,
 RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borokova D.,
 RA Miñana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
 RA Papadimitrakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
 RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,
 RA Belnert N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,
 RA Callister D.M., Campbell L.A., Darlmitou A., Henderson N.S.,
 RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
 RA Clover D.M.;
 RT "From sequence to chromosome: the tip of the X chromosome of D.
 melanogaster.";
 RT Science 287:2220-2222(2000).
 RL [5]
 RP SEQUENCE OF 2505-2611 FROM N.A.
 RX MEDLINE=85099329; PubMed=2981631;
 RA Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.;
 RT "opa: a novel family of transcribed repeats shared by the Notch locus
 and other developmentally regulated loci in D. melanogaster.";
 RT Cell 40:55-62(1985).
 RL [6]
 RP SEQUENCE OF 1-8 FROM N.A.
 RX MEDLINE=87257846; PubMed=3037327;
 RA Kelley M.R., Kidd S., Berg R.U., Young M.W.;
 RT "Restriction of P-element insertions at the Notch locus of Drosophila
 melanogaster.";
 RT Mol. Cell. Biol. 7:1545-1548(1987).
 RL [7]
 RP REVIEW.
 RA Harris W.A.;
 RT "Many cell types specified by Notch function.";
 RT Curr. Biol. 1:120-122(1991).
 RL [8]
 RP FUNCTION: Functions as a receptor for membrane-bound ligands Delta
 and Serrate to regulate cell-fate determination. Upon ligand
 activation through the released notch intracellular domain (NICD)
 it forms a transcriptional activator complex with Su(H)
 (Suppressor of hairless) and activates genes of the enhancer of
 split locus. Essential for proper differentiation of ectoderm.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
 CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
 CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
 CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
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 or send an email to license@isb-sib.ch).
 DR EMBL: M16152; AAB59220.1; -;
 DR EMBL: M16153; AAB59220.1; JOINED.

DR EMBL: M16149; AAB59220.1; JOINED.
 DR EMBL: M16150; AAB59220.1; JOINED.
 DR EMBL: M16151; AAB59220.1; JOINED.
 DR EMBL: K03508; AAA28725.1; JOINED.
 DR EMBL: M13689; AAA28725.1; JOINED.
 DR EMBL: K03507; AAA28725.1; JOINED.
 DR EMBL: AE003426; AAF45848.2; JOINED.
 DR EMBL: AL035436; CAB37610.1; JOINED.
 DR EMBL: AL035395; CAB37610.1; JOINED.
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 DR EMBL: M16025; AAA28726.1; JOINED.
 DR PIR: A24420; A24420.
 DR PIR: A24768; A24768.
 DR PIR: A05267; A05267.
 DR HSP: P00740; IEDM.
 DR Flybase: FBgn0004647; N.
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 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF-2.
 DR InterPro: IPR001881; EGF_CA.
 DR InterPro: IPR001438; EGF_II.
 DR InterPro: IPR002049; laminin_EGF.
 DR InterPro: IPR000800; Notch.
 DR Pfam: PF00008; EGF_36.
 DR Pfam: PF00023; ank; 6.
 DR Pfam: PF00066; notch; 3.
 DR PRINTS: PR00010; EGFBL00D.
 DR PRINTS: PR00011; EGFBLAMIN.
 DR PRINTS: PR01452; NOTCH.
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 DR SMART: SM00181; EGF; 36.
 DR SMART: SM00179; EGF_CA; 35.
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 DR PROSITE: PS50088; ANK_REPEAT; 5.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 22.
 DR PROSITE: PS00022; EGF_1; 34.
 DR PROSITE: PS01186; EGF_2; 28.
 DR PROSITE: PS01187; EGF_CA; 21.
 DR PROSITE: PS01187; EGF_CA; 21.
 KW Receptor; Transcription regulation; Activator; Differentiation;
 KW Developmental protein; Neurogenesis; Repeat; ANK repeat;
 KW EGF-like domain; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 44
 FT CHAIN 45 2703
 FT DOMAIN 45 1745
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Best Local Similarity 29.2%; Pred. No. 27;
 Matches 7; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
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 AC P31695; Q62389; Q62390; Q35442; Q9R1W9; O88314; O88316; Q9R1X0;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neurogenic locus notch homolog protein 4 precursor (Notch 4)
 GN NOTCH4 OR INT3 OR INT-3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NBT1;TaxID=10090;
 RN [1]
 RP MEDLINE FROM N.A.
 RX MEDLINE-92194507; PubMed-1312643;
 RA Robbins J., Blondel B.J., Gallahan D., Callahan R.;
 RT "Mouse mammary tumor gene int-3: a member of the notch gene family
 RL transforms mammary epithelial cells.";
 RU J. VIROL. 66:2594-2599(1992).
 RN [2]
 RP REVISIONS, SEQUENCE FROM N.A.
 RX MEDLINE-97294599; PubMed-9150355;
 RA Gallahan D., Callahan R.;
 RT "The mouse mammary tumor associated gene INT3 is a unique member of
 RL the NOTCH gene family (NOTCH4).";
 RU Oncogene 14:1883-1890(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Lung, and Testis;
 RC MEDLINE-96281668; PubMed-8681805;
 RA Uyttendaele H., Marrazzi G., Wu G., Yan Q., Sassoon D., Kitajewski J.;
 RT "Notch4/int-3, a mammary proto-oncogene, is an epithelial
 RL cell-specific mammalian Notch gene.";
 RU Development 122:2251-2259(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,
 RA Loretz C., Schmidt S., Tipton S., Tralcoff R., Zackrone K., Hood L.;
 RT "Sequence of the mouse major histocompatibility locus class III
 RL region.";
 RU Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1436-1600 FROM N.A.
 RX MEDLINE-99252212; PubMed-10233982;
 RA Lee J.-S., Haruna T., Ishimoto A., Honjo T., Yanagawa S.-I.;
 RT "Intracisternal type A particle-mediated activation of the Notch4/int3
 RL gene in a mouse mammary tumor: generation of truncated Notch4/int3
 RN mRNAs by retroviral splicing events.";
 RU J. VIROL. 73:5166-5171(1999).
 RN [6]
 RP FUNCTION.
 RX MEDLINE-21244657; PubMed-11344305;
 RA Uyttendaele H., Ho J., Rossant J., Kitajewski J.;
 RT "Vascular patterning defects associated with expression of activated
 RL Notch4 in embryonic endothelium.";
 RU Proc. Natl. Acad. Sci. U.S.A. 98:5643-5648(2001).
 RN [7]
 RP SEQUENCE OF 1463-1964, POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS
 RP OF VAL-1463.
 RX MEDLINE-21523956; PubMed-11518718;
 RA Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
 RT "Murine notch homologs (N1-4) undergo presenilin-dependent
 RL proteolysis.";

RL J. Biol. Chem. 276:40268-40273(2001).
RN [8]
RP POST-TRANSLATIONAL PROCESSING.
RX MEDLINE-21374376; PubMed-1145941;
RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
RT "Conservation of the biochemical mechanisms of signal transduction
among mammalian Notch family members.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands
Jagged1, Jagged2 and Delta to regulate cell-fate determination.
Upon ligand activation through the released notch intracellular
domain (NICD) it forms a transcriptional activator complex with
RBP-J kappa and activates genes of the enhancer of split locus.
Affects the implementation of differentiation, proliferation and
apoptotic programs (By similarity). May regulate branching
morphogenesis in the developing vascular system.
CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
terminal fragment N(EC) which are probably linked by disulfide
bonds.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following
proteolytic processing NICD is translocated to the nucleus.
CC -1- TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart
kidney, and at lower levels in the ovary and skeletal muscle. A
very low expression is seen in the brain, intestine, liver and
testis.
CC -1- DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during
embryonic development from 9.0 d.p.c.
CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form
which is proteolytically cleaved by a furin-like convertase in the
trans-golgi network before it reaches the plasma membrane to yield
an active, ligand-accessible form. Cleavage results in a C-
terminal fragment N(TM) and a N-terminal fragment N(EC). Following
ligand binding, it is cleaved by TNF-alpha converting enzyme
(TACE) to yield a membrane-associated intermediate fragment called
notch extracellular truncation (NEXT). This fragment is then
cleaved by presenilin dependent gamma-secretase to release a
notch-derived peptide containing the intracellular domain (NICD)
from the membrane.
CC -1- PTM: Phosphorylated.
CC -1- DISEASE: Loss of the extracellular domain causes constitutive
activation of the Notch protein, which leads to hyperproliferation
of glandular epithelial tissues and development of mammary
carcinomas.
CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
CC -1- SIMILARITY: CONTAINS 29 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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or send an email to license@isb-slb.ch)
CC -----
DR EMBL: M80456; AAB3837.1; -
DR EMBL: U43691; AAC52630.1; -
DR EMBL: U43691; AAC52631.1; -
DR EMBL: AF030001; AAB82004.1; -
DR EMBL: AB016771; BAA32281.1; ALT_SEQ.
DR EMBL: AB016772; BAA32283.1; ALT_INIT.
DR EMBL: AB016773; BAA32284.1; ALT_INIT.
DR EMBL: AB016774; BAA32285.1; -
DR PIR: A38072; TVMW3.
DR HSSP: P08709; 1BF9.
DR MGD: MGI:107471; Notch4.
DR InterPro: IPR002110; Notch4.
DR InterPro: IPR000152; ANK.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF-2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.

DR InterPro: IPR000800; Notch.
DR Pfam: PF00008; EGF; 27.
DR Pfam: PF00023; ank; 6.
DR Pfam: PF00066; notch; 2.
DR PRINTS: PR01415; ANKYRN.
DR PRINTS: PR00010; EGRBLOOD.
DR PRINTS: PR01452; NOTCH.
DR SMART: SM00248; ANK; 5.
DR SMART: SM00179; EGF_CA; 11.
DR SMART: SM00001; EGF_Like; 15.
DR SMART: SM00004; NL; 2.
DR PROSITE: PS50088; ANK_REPEAT; 5.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 11.
DR PROSITE: PS00022; EGF_1; 28.
DR PROSITE: PS01186; EGF_2; 21.
DR PROSITE: PS01187; EGF_CA; 9.
DR Receptor, Transcription regulation; Activator; Differentiation;
Developmental protein; Repeat; ANK repeat; EGF-like domain;
Transmembrane; Glycoprotein; Signal; Phosphorylation; Proto-oncogene.
KW SIGNAL 1
KW CHAIN 21
KW CHAIN 21
KW CHAIN 1411
KW CHAIN 1428
KW CHAIN 1463
KW CHAIN 1463
KW TRANSMEM 21
KW DOMAIN 1444
KW DOMAIN 1465
KW DOMAIN 1464
KW DOMAIN 21
KW DOMAIN 61
KW DOMAIN 115
KW DOMAIN 153
KW DOMAIN 191
KW DOMAIN 231
KW DOMAIN 273
KW DOMAIN 311
KW DOMAIN 352
KW DOMAIN 389
KW DOMAIN 429
KW DOMAIN 472
KW DOMAIN 510
KW DOMAIN 548
KW DOMAIN 586
KW DOMAIN 623
KW DOMAIN 658
KW DOMAIN 688
KW DOMAIN 726
KW DOMAIN 764
KW DOMAIN 803
KW DOMAIN 841
KW DOMAIN 878
KW DOMAIN 926
KW DOMAIN 964
KW DOMAIN 1002
KW DOMAIN 1042
KW DOMAIN 1083
KW DOMAIN 1126
KW DOMAIN 1168
KW REPEAT 1209
KW REPEAT 1243
KW REPEAT 1282
KW REPEAT 1628
KW REPEAT 1651
KW REPEAT 1691
KW REPEAT 1724
KW REPEAT 1728
KW SIGNAL 20
KW CHAIN 1964
KW CHAIN 1964
KW CHAIN 1964
KW CHAIN 1964
KW CHAIN 1964
KW TRANSMEM 1444
KW DOMAIN 1465
KW DOMAIN 1964
KW DOMAIN 60
KW EGF-LIKE 1
KW EGF-LIKE 2
KW EGF-LIKE 3
KW EGF-LIKE 4
KW EGF-LIKE 5
KW EGF-LIKE 6
KW EGF-LIKE 7
KW EGF-LIKE 8
KW EGF-LIKE 9
KW EGF-LIKE 10
KW EGF-LIKE 11
KW EGF-LIKE 12
KW EGF-LIKE 13
KW EGF-LIKE 14
KW EGF-LIKE 15
KW EGF-LIKE 16
KW EGF-LIKE 17
KW EGF-LIKE 18
KW EGF-LIKE 19
KW EGF-LIKE 20
KW EGF-LIKE 21
KW EGF-LIKE 22
KW EGF-LIKE 23
KW EGF-LIKE 24
KW EGF-LIKE 25
KW EGF-LIKE 26
KW EGF-LIKE 27
KW EGF-LIKE 28
KW EGF-LIKE 29
KW LIN/NOTCH 1
KW LIN/NOTCH 2
KW LIN/NOTCH 3
KW ANK 1
KW ANK 2
KW ANK 3
KW ANK 4
Query Match Similarity 54.2%; Score 65; DB 1; Length 1964;
Best Local 33.3%; Pred. No. 26;
Matches 7; Conservative 12; Mismatches 2; Indels 0; Gaps 0;
QY 7 XCXQXLDCCSXCNXKNXCV 27
DB 348 GCENLDDCAANATCAPGSTCI 368

Search completed: January 14, 2003, 18:31:05
Job time : 13 secs

* * *

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 18:29:32 ; Search time 28 Seconds

(without alignments)
198,688 Million cell updates/sec

Title: US-09-666-837b-1

Perfect score: 120

Sequence: 1 CXIXNKCXQXLDCCSXKXNXCVCV 27

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55.8	778	13	Q9IBG4	Q9IBG4 xenopus lae
2	55.8	2146	5	Q9VC97	Q9VC97 drosophila
3	55.0	664	5	Q9IAR6	Q9IAR6 brachydanio
4	55.0	721	13	Q91902	Q91902 xenopus lae
5	55.0	1551	5	Q9NGV4	Q9NGV4 drosophila
6	55.0	2447	13	Q13149	Q13149 fugu rubrip
7	55.0	3396	5	Q9VM55	Q9VM55 drosophila
8	54.2	752	13	Q42374	Q42374 brachydanio
9	54.2	1075	5	Q9NC90	Q9NC90 strongyloce
10	54.2	1214	13	Q90YD2	Q90YD2 xenopus lae
11	54.2	1290	5	Q9W6E1	Q9W6E1 gallus gall
12	54.2	1440	5	Q20204	Q20204 caenorhabdi
13	54.2	2531	5	Q16004	Q16004 lytechinus
14	54.2	2653	5	Q25253	Q25253 lucilia cup
15	53.3	838	5	Q9YQAG	Q9YQAG drosophila
16	53.3	1372	5	P91526	P91526 caenorhabdi

17	64	53.3	2352	5	Q61240	Q61240 halocynthia
18	64	53.3	3623	11	Q70244	Q70244 rattus norv
19	63	52.5	642	13	P79941	P79941 xenopus lae
20	63	52.5	1687	11	Q61204	Q61204 mus musculus
21	62	51.7	153	10	Q9AUD1	Q9AUD1 sesamum ind
22	62	51.7	204	4	Q9B054	Q9B054 homo sapien
23	62	51.7	713	5	Q962W9	Q962W9 podocoryne
24	62	51.7	723	4	Q9UJV2	Q9UJV2 homo sapien
25	62	51.7	723	4	Q9NU41	Q9NU41 homo sapien
26	62	51.7	1515	13	Q9PD37	Q9PD37 brachydanio
27	62	51.7	1685	5	Q9U4A2	Q9U4A2 plasmodium
28	62	51.7	2324	5	Q9GPA5	Q9GPA5 brachydanio
29	61.5	51.2	81	5	Q9BP77	Q9BP77 conus arena
30	61.5	51.2	471	10	Q8VZ55	Q8VZ55 arabidopsis
31	61.5	51.2	481	10	Q9ZVY7	Q9ZVY7 arabidopsis
32	61	50.8	66	5	Q9M6P8	Q9M6P8 conus catus
33	61	50.8	66	5	Q9M6P8	Q9M6P8 conus catus
34	61	50.8	66	5	Q9M6P8	Q9M6P8 conus catus
35	61	50.8	463	10	Q9AMX7	Q9AMX7 oryza sativ
36	61	50.8	530	5	Q24526	Q24526 drosophila
37	61	50.8	728	13	Q90656	Q90656 gallus gall
38	61	50.8	1025	11	Q92166	Q92166 mus musculus
39	61	50.8	1216	13	Q90Y55	Q90Y55 brachydanio
40	61	50.8	1254	13	Q9YHU2	Q9YHU2 brachydanio
41	61	50.8	1254	13	Q90Y56	Q90Y56 brachydanio
42	61	50.8	1316	4	Q96J07	Q96J07 homo sapien
43	61	50.8	1404	5	Q9VB65	Q9VB65 drosophila
44	61	50.8	1480	5	Q9V7P8	Q9V7P8 drosophila
45	61	50.8	1504	5	Q9XYV4	Q9XYV4 drosophila

ALIGNMENTS

RESULT 1	Q9IBG4	PRELIMINARY:	PRT:	778 AA.
AC	Q9IBG4:			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Secretory protein containing EGF domain precursor.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20245325; PubMed=10781962;			
RA	Kuriyama S., Miyatani S., Kinoshita T.;			
RT	"Xerl; a novel secretory protein expressed in eye and brain of Xenopus			
RT	embryo.";			
RL	Mech. Dev. 93:233-237(2000).			
DR	EMBL: AB027453; BAA95001.1; -.			
DR	HSSP: P08709; IEP9.			
DR	InterPro: IPR000152; Asx_hydroxyl.			
DR	InterPro: IPR000561; EGF-like.			
DR	InterPro: IPR000742; EGF_2.			
DR	InterPro: IPR001881; EGF_Ca.			
DR	InterPro: IPR001438; EGF_T1.			
DR	InterPro: IPR002049; Laminin_EGF.			
DR	InterPro: IPR001791; Laminin_G.			
DR	Pfam: PF00008; EGF_13.			
DR	Pfam: PF00054; Laminin_G: 1.			
DR	PRINTS: PR00010; EGFLOD.			
DR	PRINTS: PR00011; EGFAMININ.			
DR	SMART: SM00179; EGF_CA: 6.			
DR	SMART: SM00282; EGF_Like: 7.			
DR	PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_7.			
DR	PROSITE: PS00022; EGF_1; UNKNOWN_10.			
DR	PROSITE: PS0186; EGF_2; 10.			

DR	PROSITE PS01187; EGF CA; 6.
KM	Calcium-binding; EGF-like domain; Glycoprotein; Repeat; Signal.
FT	SIGNAL I 27 POTENTIAL.
SO	SEQUENCE 778 AA; 85516 MW; 462D2C84AE435CF6 CRC64;
OY	4 XNQCXQXALDDCCSXXKXNXC V 27
Dy	: ::::: : : : : :
Db	285 DDELQQDDIDECQSQPCNGRCV 308
RESULT 2	
O9VC97	PRELIMINARY: PRT: 2146 AA.
ID	O9VC97
AC	O9VC97;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	Crb protein
CN	Crb OR C6G583.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxId=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-BERKELEY;
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Gelinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R.C., Yandell M.D., Zhang Q., Chen L.X.,
RA	Barton R.C., Rogers Y.H.C., Blazer R.G., Chapple M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abdill J.F., Agbayani A.A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA	Ballaw R.M., Basu A.A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benton P.V., Bereman B.P., Bhattacharya D., Bolshakov S.,
RA	Bortone D., Botchan M.R., Bouck J., Brocktein P., Brotter P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cavley S., Dahlke C., Davernport L.B., Davies P.,
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doul L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA	Foster C., Garfield A.E., Gang N.S., Gelbart W.M., Glasser K.,
RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA	Jailai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulip D., Lai Z.,
RA	Lasro P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merulov G., Mishina N.V., Mobarry C., Morris J., Mostreft A.,
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA	Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Paetle J.M.,
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA	Shue B.C., Sidenkiamos I., Simpson M., Skupski M.P., Smith T.,
RA	Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
RA	Switkska R., Teichor C., Turner R., Venler E., Wang A.H., Wang X.,
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA	Williams R.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA	Ye J., Yeh R.-F., Zaveril J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT	"The genome sequence of Drosophila melanogaster." ;
RL	Science 287:2185-2195(2000).
EMBL	AE003747; AAF56276.1; -.
DR	HSSP: P00740; IEDEM.
DR	Physpe: FBgn0000368; crfb.

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DR InterPro: IPR000152; Asx_hydroxyl-
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR001791; Laminin_G.
DR Pfam: PF00008; EGF_26.
DR Pfam: PF00054; laminin_G; 3.
DR PRINTS: PR00010; EGFBLDOD.
DR PRINTS: PR00011; EGFLAMININ.
DR SMART: SM00179; EGF_CA; 11.
DR SMART: SM00001; EGF_like; 16.
DR SMART: SM00282; LamG; 3.
DR PROSITE: PS00010; ASX_HYDROXYL; 16.
DR PROSITE: PS00022; EGF_1; 25.
DR PROSITE: PS01186; EGF_2; 17.
DR PROSITE: PS01187; EGF_CA; 13.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SQ SEQUENCE 2146 AA; 233570 MW; 8E23B9B532B76115 CRC64;

Query Match 55.8%; Score 67; DB 5; Length 2146;
Best Local Similarity 28.0%; Pred. No. 4.1;
Matches 7; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

QY 2 XIXNQXCXXOXIDDCSCXXCNKXNXC 26
DB 1823 GREGHCEQNIDECAQCPCNHNGNC 1847
      :|::||::||::|::|
      :|::||::||::|::|

RESULT 3
O9IAT6 PRELIMINARY; PRT; 664 AA.
AC O9IAT6;
DT 01-OCT-2000 (TREMBLrel. 15; Created)
DT 01-OCT-2000 (TREMBLrel. 15; Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19; Last annotation update)
GN Delcac.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Butelostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
CX NCBI_TaxID=7955;
RN [1]
RP MEDLINE=20054100; PubMed=10585570;
RX Smithers L.E., Haddon C., Jiang Y.-J., Lewis J.;
RT "Sequence and embryonic expression of delcac in the zebrafish.";
RL Mech. Dev. 90:119-123(2000).
DR EMBL: AF164429; AAF27299.1; -.
DR HSPF: P00740; IEDM.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001774; DSL.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR002049; Laminin_EGF.
DR Pfam: PF01414; DSL; 1.
DR Pfam: PF00008; EGF; 1.
DR PRINTS: PR00010; EGFBLDOD.
DR PRINTS: PR00011; EGFLAMININ.
DR SMART: SM00051; DSL; 1.
DR SMART: SM00179; EGF_CA; 4.
DR SMART: SM00001; EGF_like; 4.
DR PROSITE: PS00022; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE: PS00010; EGF_1; UNKNOWN_8.
DR PROSITE: PS01186; EGF_2; 8.
DR PROSITE: PS01187; EGF_CA; 2.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SQ SEQUENCE 664 AA; 72547 MW; 0AD6C34C85791168 CRC64;

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Query Match          55.0%: Score 66; DB 13; Length 664;
Best Local Similarity 30.8%; Pred.No. 1.9;
Matches      8; Conservative    11; Mismatches     7; Indels     0; Gaps     0;

OY      2 X1XNQXCXQXLDDCCSXKCNXXNCV 27
       : : : : : ||| | : : : : ||
Db       411 GFPGSRCEFTNIDCSSNPCQNAGTCV 436

RESULT 4
OY1902   PRELIMINARY; PRT; 721 AA.
AC OY1902:
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE x-delta-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95319507; PubMed=7596411;
RX Chitnits A., Henrique D., Lewis J., Ish-Horowitz D., Kintner C.;
RT "Primary neurogenesis in xenopus embryos regulated by a homologue of
RL the Drosophila neurogenic gene delta.";
RL Nature 375:761-766(1995);
DR EMBL: L42229; AAC38017.1; -.
DR HSSP; P00740; IEDM.
DR InterPro; IPRO00152; Asx_hydroxyl.
DR InterPro; IPRO01774; DSL.
DR InterPro; IPRO00561; EGF_1-like.
DR InterPro; IPRO00742; EGF_2.
DR InterPro; IPRO01881; EGF_Ca.
DR InterPro; IPRO01436; EGF_IT.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 8.
DR PRINTS; PR00010; EGFBLDOD.
DR SMART; SM00551; DSL; 1.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00001; EGF_like; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_3.
DR PROSITE; PS00022; EGF_1; UNKNOWN_8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS01187; EGF_CA; 2.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SQ SEQUENCE 721 AA; 79922 MM; 9EBDC85C439DD194 CRC64;

Query Match          55.0%: Score 66; DB 13; Length 721;
Best Local Similarity 32.0%; Pred.No. 2.1;
Matches      8; Conservative    11; Mismatches     6; Indels     0; Gaps     0;

OY      2 X1XNQXCXQXLDDCCSXKCNXXNCV 26
       : : : : : ||| | : : : : ||
Db       436 GFSGRNDNDNLDCSTFPCQNGGTC 460

RESULT 5
OY1902   PRELIMINARY; PRT; 1551 AA.
AC OY1902:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

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DE SPI070. OR CG9138.
GN
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Neozoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN
RP
RP SEQUENCE FROM N.A.
RC TISSUE=ENDOPLEASMIC RETICULUM;
RA Serano T.L., Pendleton J.D., Rubin G.M.;
RT "A reverse genetic screen for genes involved in Drosophila
RT development."
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF239608; AAF63500.1; -.
DR HSSP: P00740; 1EDM.
DR FlyBase; FBgn0031879; SPI070.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR003410; Hyalin.
DR InterPro: IPR002049; LamAin_EGF.
DR InterPro: IPR001791; LamAin_G.
DR InterPro: IPR002172; LDL_recept_A.
DR Pfam: PF00008; EGF_16.
DR Pfam: PF02494; HVR_1.
DR PRINTS: PRO0010; EGFALOOD.
DR PRINTS: PRO0011; EGFAMININ.
DR SMART: SM00179; EGF_CA; 6.
DR SMART: SM00001; EGF_1like; 9.
DR SMART: SM00282; LamG; 1.
DR SMART: SM00192; LDLA; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_9.
DR PROSITE: PS00022; EGF_1; UNKNOWN_15.
DR PROSITE: PS01186; EGF_2; 12.
DR PROSITE: PS01187; EGF_CA; 5.
DR Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
DR KW SEQUENCE 1551 AA; 167816 MW; A97EA229E9384F31 CnC64;
SQ

Query Match 55.0%; Score 66; DB 5; Length 1551;
Best Local Similarity 33.3%; Pred. No. 4.1;
Matches 8; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 4 XNQCXQXLDNCCSXNKNXXNCV 27
      :::: :||| :||| :::: ||
Db 278 TGRKCGHTIDDCASNFCQGATCV 301

RESULT 6
O13149 PRELIMINARY; PRT; 2447 AA.
ID O13149
AC O13149;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DS Notch 2 (Fragment).
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OC NCBI_TaxID=31033;
OX NOBI_TaxID=31033;
RN
RP
RP SEQUENCE FROM N.A.
RA Nakamura T., Trowsdale J.;
RT "Structure of Fugu Notch gene."
RL Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB004829; BAA20535.1; -.
DR HSSP: P00740; 1EDM.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000152; Asx_hydroxyl.

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DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_CA.
 DR InterPro: IPR001438; EGF_11.
 DR InterPro: IPR000083; Fibronctn1.
 DR InterPro: IPR002049; Lamlnln_EGF.
 DR InterPro: IPR000800; Notch.
 DR Pfam: PF000023; ank; 6.
 DR Pfam: PF00008; EGF_35.
 DR Pfam: PF00066; notch; 3.
 DR PRINTS: PR00010; EGFBL00D.
 DR PRINTS: PR00011; EGFBLAMININ.
 DR PRINTS: PR00012; FNTYPEI.
 DR SMART: SM00248; ANK; 5.
 DR SMART: SM00179; EGF_CA; 20.
 DR SMART: SM00001; EGF_Like; 14.
 DR SMART: SM00004; NL; 3.
 DR PROSITE: PS50088; ANK_REPEAT; 8.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 2.
 DR PROSITE: PS00010; ASX_HYDROXYL; 22.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_35.
 DR PROSITE: PS01186; EGF_2; 29.
 DR PROSITE: PS01187; EGF_CA; 20.
 DR ANK repeat; Calcium-binding; EGF-like domain; Glycoprotein;
 KM Hydroxylation; Repeat.
 FT NON_TER
 SQ SEQUENCE 2447 AA; 262541 MW; 1ABE2A372A085D84 CRC64;

Query Match 55.0%; Score 66; DB 13; Length 2447;
 Best Local Similarity 29.0%; Pred. No. 6.2;
 Matches 9; Conservative 15; Mismatches 3; Indels 4; Gaps 1;

Oy 1 CXIXN---OXCXQXLDCCSXXCNXXNCV 27
 Db 279 CVCVNGMSGDCCSENIDCDTAACSPGTCV 309

RESULT 7
 09YMS5 PRELIMINARY; PRT; 3396 AA.
 AC 09YMS5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE CG9138 protein.
 GN SPI070 OR CG9138.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA MEDLINE=20196006; Pubmed=1071112;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abbill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A.A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
 RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Paulis B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Rosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maltel B., McInosh T.C., McLeod K.P., McInosh D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Relbert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 CC -1- SIMILARITY: CONTAINS 3 CUB DOMAINS.
 DR EMBL: AE003615; AAF52472.1; -.
 DR HSP: P00740; 1EDM.
 DR Flybase: FBgn0031879; SPI070.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000859; CUB_domain.
 DR InterPro: IPR000561; EGF_Like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_CA.
 DR InterPro: IPR001438; EGF_11.
 DR InterPro: IPR000421; FA58_C.
 DR InterPro: IPR001092; HLH_basic.
 DR InterPro: IPR003410; Hyalin.
 DR InterPro: IPR001791; Lamlnln-G.
 DR InterPro: IPR002172; LDL_recept-A.
 DR InterPro: IPR000436; Sush1_SCR_CCP.
 DR InterPro: IPR001368; TNER_C6.
 DR Pfam: PF00431; CUB; 3.
 DR Pfam: PF00008; EGF; 17.
 DR Pfam: PF00754; F5_FB_type_C; 2.
 DR Pfam: PF02494; HVR; 3.
 DR Pfam: PF00057; Id1_recept_a; 1.
 DR Pfam: PF00084; sush1; 7.
 DR PRINTS: PR00010; EGFBL00D.
 DR SMART: SM00032; CCP; 8.
 DR SMART: SM00042; CUB; 3.
 DR SMART: SM000179; EGF_CA; 8.
 DR SMART: SM00001; EGF_Like; 9.
 DR SMART: SM00231; FA58C; 2.
 DR SMART: SM00192; LamG; 1.
 DR SMART: SM00192; LDLA; 1.
 DR SMART: SM00208; TNER; 2.
 DR PROSITE: PS00010; ASX_HYDROXYL; 11.
 DR PROSITE: PS01180; CUB; 6.
 DR PROSITE: PS00022; EGF_1; 15.
 DR PROSITE: PS01186; EGF_2; 13.
 DR PROSITE: PS01187; EGF_CA; 7.
 DR PROSITE: PS01285; FA58C_1; 1.
 DR PROSITE: PS01209; LDLRA_1; 1.
 DR PROSITE: PS50068; LDLRA_2; 2.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
 SQ SEQUENCE 3396 AA; 369389 MW; B618B9ACEA13E0E5 CRC64;

Query Match 55.0%; Score 66; DB 5; Length 3396;
 Best Local Similarity 33.3%; Pred. No. 8.3;
 Matches 8; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Oy 4 XNQCXQXLDCCSXXCNXXNCV 27
 Db 2119 TGRNCGHTIDCASNPCGATGATCV 2142

RESULT 8

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042374
ID 042374 PRELIMINARY; PRT: 752 AA.
AC 042374;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Notch receptor protein (Fragment).
GN NOTCH2 OR NOTCH6.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Westin J., Lardelli M.;
RT "Three novel Notch genes in zebrafish: implications for vertebrate
RT Notch gene evolution and function.";
RL Dev. Genes Evol. 207:51-63(1997).
DR EMBL: Y10354; CAA71380.1; -.
DR HSSP: P00740; 1EDM.
DR ZFIN: ZDB-GENE-000329-4; notch2.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_11.
DR InterPro: IPR000083; Fibrinctn1.
DR InterPro: IPR002049; laminin_EGF.
DR InterPro: IPR000800; Notch.
DR Pfam: PF00008; EGF_16.
DR Pfam: PF00066; notch_2.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR00011; EGFBL00D.
DR PRINTS: PR00012; FNTYPE1.
DR SMART: SM00179; EGF_CA; 9.
DR SMART: SM00001; EGF_Like; 5.
DR SMART: SM00004; NL_2.
DR PROSITE: PS00010; ASX_HYDROXYL; 9.
DR PROSITE: PS00022; EGF_1; UNKNOWN_17.
DR PROSITE: PS01186; EGF_2; 15.
DR PROSITE: PS01187; EGF_CA; 7.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;
KW Receptor; Repeat.
FT NON_TER 1
FT NON_TER 752
SQ SEQUENCE 752 AA; 82103 MW; 30939E16E0327F8A CRC64;

Query Match 54.2%; Score 65; DB 13; Length 752;
Best local Similarity 33.3%; Pred. No. 2.9;
Matches 8; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 4 XNQCXQXILDCCSXKXNKNXCV 27
DB 132 SGDNCQTHIDCSSNFCRNGTCV 155

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RA Panzer Z.;
RT "Dynamic expression of multiple scavenger receptor cysteine-rich genes
RT in coelomocytes of the purple sea urchin.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:13156-13161(2000).
DR EMBL: AF228824; AAF76316.1; -.
DR HSSP: P00740; 1EDM.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_11.
DR InterPro: IPR001190; Srcr_receptor.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR Pfam: PF00008; EGF_3.
DR Pfam: PF00530; SRCR_7.
DR Pfam: PF00084; sushi_1.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR00258; SPERACTRCPTR.
DR SMART: SM00332; CCP; 1.
DR SMART: SM00179; EGF_CA; 2.
DR SMART: SM00001; EGF_Like; 1.
DR SMART: SM00202; SR; 6.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE: PS00022; EGF_1; UNKNOWN_2.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE: PS00420; SRCR_1; UNKNOWN_3.
DR PROSITE: PS0287; SRCR_2; 7.
KW EGF-like domain; Glycoprotein; Receptor.
SQ SEQUENCE 1075 AA; 116178 MW; 61395AD6FD30BA3D CRC64;

Query Match 54.2%; Score 65; DB 5; Length 1075;
Best local Similarity 33.3%; Pred. No. 4;
Matches 8; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 4 XNQCXQXILDCCSXKXNKNXCV 27
DB 862 TGSSCDTEIDCSSSPCGDNGVCV 885

RESULT 10
Q90YD2 PRELIMINARY; PRT: 1214 AA.
AC Q90YD2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE X-serrate-1 protein.
GN X-SERRATE-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kiyota T., Jono H., Kuriyama S., Hasegawa K., Miyatani S.,
RA Kinoshita T.;
RT "X-serrate-1 is involved in primary neurogenesis in Xenopus laevis in
RT a complementary manner with X-Delta-1.";
RL Dev. Genes Evol. 211:367-376(2001).
DR EMBL: AB027537; BAB59049.1; -.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001774; DSL.
DR InterPro: IPR000561; EGF_Like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001007; VWF_C.
DR Pfam: PF01414; DSL; 1.
DR Pfam: PF00008; EGF_14.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_10.
DR PROSITE: PS00022; EGF_1; UNKNOWN_16.

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DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Notch homolog scalloped wings (SCL).

05 *Lucilia cuprina* (Greenbottle fly) (Australian sheep blowfly).
0C Eukaryota; Metazoa; Arthropoda; Trachata; Hexapoda; Insecta;
0C Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

RN	[1]
RP	SEQUENCE FROM N.A.

```
RC STRAIN=SS SEEKING;
      *****
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RA Davies A.G., Game A.Y., Chen Z., Williams T.J., Goodall S., Yen J.L.,
RA McKenzie T.A., Rattray P.

"Scalloped wings is the *Lucilia cuprina* Notch homologue and a

RT resistance.", and model of fitness and asymmetry of virulence

GENETICS 143:1321-1337 (1956)
[2]
REFERENCE OF 20 OCT. 1956

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RC STRAIN=SS SEEKING;
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Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases

RN [3]
RD SEQUENCE OF 39-265 FROM N 2

RC STRAIN=SS SEEKING;
RA Chen Z., McKenzie J.A., Batterham P.;

Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases
EMBL: U589977; AAC36151.1; -

DR EMBL; AF032672; AAC36152.1; -
EMBL; AF032670; AAC36153.1; -
EMBL; AF032671; AAC36154.1; -

DR EMBL; AF032671; AAC36152.1; JOINED.

DR *EMBL*; AF032075; AAC30133.1; .
DR HSSP; P00740; 1EDM.
DR

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DR InterPro: IPR002110; ANK.  
DR InterPro: IPR000153; Asy_hydroxyl
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DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF_Ca.

DR	InterPro; IPR001436; EGF_11.
DR	InterPro; IPR000800; Notch.

DR Pfam: PF00023; ank; 6.
DR Pfam: PF00008; EGF; 35

DR Pfam; PF00066; notch; 3.

PRINTS; PR01452; NOTCH.

DR SMART; SM00179; EGF CA: 24.
DR SMART; SM00248; ANK; 4.

DR SMART; SM000001; EGF-like; 11.
DR SMART; SM000004; NI; 3

DR PROSITE; PS50088; ANK_REPEAT; 5.

DR PROSITE; PS00010; ASX_HYDROXYL; 22.

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DR PROSITE: PS00022; EGF_1; UNKNOWN_34.
DR PROSITE: PS01186; EGF_2; 28.
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DR PROSITE; PS01187; EGF_CA; 21.

Hydroxylation; Repeat.

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Best Local Similarity	29.28;	Pred. No. 8.9;		

Matches 7; Conservative 12; Mismatches 5; Indel

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Db 268 QGKNCEQNIDDCPGHLCQNGGTCT 291

RESULT: 15
09V0A9

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PRT;		

DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE CG15388 protein.
 GN CG15388
 OS Drosophila melanogaster (Fruit fly)
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID:7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abirl J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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 RA Burlis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
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 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Klumel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003583; AAF51268.1; -.
 DR HSP: P00740.1EDM.
 DR FLYBase; FBgn0031414; CG15388.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF-2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_TL.
 DR InterPro: IPR002965; P_rich_extensn.
 DR Pfam; PF00008; EGF; 5.
 DR PRINTS; PRO0010; EGFBL00D.
 DR PRINTS; PRO1217; PRICHEXTNSN.
 DR SMART; SM00179; EGF_CA; 3.
 DR SMART; SM00001; EGF_like; 2.
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 DR PROSITE; PS00022; EGF_1; 5.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 3.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
 SQ SEQUENCE 838 AA; 87786 MW; A654CDBE4FDF42B0 CRC64;

Query Match 53.3%; Score 64; DB 5; Length 838;
 Best Local Similarity 28.0%; Pred. No. 4.3;
 Matches 7; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

QY 2 XINQXCXOXLDCCSCXCNXNXC 26
 DB 4 EIKSNCEENVDCMSNPQNGGLC 28

Search completed: January 14, 2003, 18:31:41
 Job time : 30 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 18:16:30 ; Search time 35 Seconds
(without alignments)
102.793 Million cell updates/sec

Title: US-09-666-837b-1-COPY
Perfect score: 140
Sequence: 1 CRIXMOKCQHIDCCSXKXNXXCV 27 }

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
24: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	129	92.1	27	AAU10196	Snail Kappa-conoto
2	129	92.1	27	AAU10197	Snail Kappa-conoto
3	129	92.1	27	AAU10199	Snail Kappa-conoto
4	129	92.1	27	AAU10202	Snail Kappa-conoto
5	129	92.1	27	AAU10218	Snail Kappa-conoto
6	127	90.7	27	AAU35723	Kappa-conotoxin PV
7	125	89.3	27	AAU10203	Snail Kappa-conoto
8	125	89.3	27	AAU10206	Snail Kappa-conoto
9	125	89.3	27	AAU10212	Snail Kappa-conoto
10	124	88.6	27	AAU10207	Snail Kappa-conoto

11	124	88.6	27	AAU10217	Snail Kappa-conoto
12	123	87.9	27	AAU10198	Snail Kappa-conoto
13	123	87.9	27	AAU10214	Snail Kappa-conoto
14	122	87.1	27	AAU10200	Snail Kappa-conoto
15	122	87.1	27	AAU10204	Snail Kappa-conoto
16	122	87.1	27	AAU10205	Snail Kappa-conoto
17	122	87.1	27	AAU10210	Snail Kappa-conoto
18	122	87.1	27	AAU10216	Snail Kappa-conoto
19	120	85.7	27	AAU10201	Snail Kappa-conoto
20	120	85.7	27	AAU10209	Snail Kappa-conoto
21	120	85.7	27	AAU10211	Snail Kappa-conoto
22	120	85.7	27	AAU10213	Snail Kappa-conoto
23	120	85.7	27	AAU10215	Snail Kappa-conoto
24	120	85.7	27	AAU10219	Snail Kappa-conoto
25	118	84.3	27	AAU10208	Snail Kappa-conoto
26	100	71.4	27	AAU10195	Snail Kappa-conoto
27	66	47.1	27	ABB96772	Omega-conopeptide
28	66	47.1	27	ABB96874	Omega-conopeptide
29	65	46.4	26	ABB96786	Omega-conopeptide
30	65	46.4	27	ABB96774	Omega-conopeptide
31	65	46.4	27	ABB96846	Omega-conopeptide
32	65	46.4	27	ABB96876	Omega-conopeptide
33	65	46.4	72	ABB96638	Omega-conopeptide
34	65	46.4	72	ABB96666	Omega-conopeptide
35	65	46.4	72	ABB96688	Omega-conopeptide
36	64	45.7	26	AAU37774	SNX-202. Synthet
37	64	45.7	26	AAU39628	SNX-202. Synthet
38	64	45.7	26	AAU19570	SNX-202. Synthet
39	64	45.7	26	AAU12985	Omega conopeptide
40	64	45.7	26	AAU72625	Conus genus analog
41	64	45.7	26	AAU55584	Analag omega-conop
42	64	45.7	26	AAU14370	Analag omega-conop
43	64	45.7	26	AAU56462	Analag omega con
44	64	45.7	26	AAU19462	Sequence of an ome
45	63	45.0	26	ABB96887	Omega-conopeptide

ALIGNMENTS

RESULT 1	AAU10196	standard; peptide; 27 AA.
ID	AAU10196;	
AC	AAU10196;	
XX		
DF	16-JAN-2002 (first entry)	
XX		
DE	Snail Kappa-conotoxin PY1A analogue R18A.	
XX		
KW	Purple cone snail; kappa-conotoxin PY1A analogue; circulatory;	
KW	cardioactive; antilasthmatic; KAP channel activation; cardiac ischaemia;	
KW	cerebral ischaemia; ocular ischaemia; asthma; R18A.	
XX		
OS	Conus purpurascens.	
OS	Synthetic.	
XX		
PH	Key	Location/Qualifiers
FT	Modified-site	4
FT	Modified-site	/note= "Hydroxyproline"
FT	Modified-site	27
FT	/note= "The C-terminus is either a carboxyl group or an amide group"	
XX		
XX	WO200121648-A1.	
PN		
XX		
PD	29-MAR-2001.	
XX		
PF	21-SEP-2000; 2000WO-US25827.	
XX		
PR	22-SEP-1999; 99US-155135P.	
PR	20-JUL-2000; 2000US-0219438.	
XX		

PA (COGN-) COGNETIX INC.
XX
PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
XX
DR WPI: 2001-648090/74.
XX
PT Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma
PT comprises activating a KATP channel by administering to an individual a
PT kappa-conotoxin PVIIA peptide -
XX
PS Claim 1: Page 27; 46pp; English.
XX
XX The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA
CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
CC active salt. The conotoxins are used for treating disorders associated
CC with radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischemia, cerebral ischemia, ocular
CC ischemia and asthma. The present sequence is a kappa-conotoxin
CC PVIIA analogue of the invention.
XX
SQ Sequence 27 AA:

Query Match 92.1%; Score 129; DB 22; Length 27;
Best Local Similarity 81.5%; Pred. No. 5.4e-09;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSXCNXKXCV 27
|||
DB 1 CRXNQKCFQHLDDCCSACNRFNKCV 27

RESULT 2

AAU10197
ID AAU10197 standard; peptide: 27 AA.

AC AAU10197;

DT 16-JAN-2002 (first entry)

DE Snail Kappa-conotoxin PVIIA analogue R22A.

KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;

KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischemia;

KW cerebral ischemia; ocular ischemia; asthma; R22A.

OS Conus purpurascens.

OS Synthetic.

FT Key Location/Qualifiers

FT Modified-site 4 /note= "Hydroxyproline"

FT Modified-site 27 /note= "The C-terminus is either a carboxyl group
or an amide group"

PN WO200121648-A1.

PD 29-MAR-2001.

PF 21-SEP-2000; 2000WO-US25827.

PR 22-SEP-1999; 99US-155135P.

PR 20-JUL-2000; 2000US-0219438.

PA (COGN-) COGNETIX INC.

PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;

DR WPI: 2001-648090/74.
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XX
PS Claim 1: Page 27; 46pp; English.
XX
XX The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA
CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
CC active salt. The conotoxins are used for treating disorders associated
CC with radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischemia, cerebral ischemia, ocular
CC ischemia and asthma. The present sequence is a kappa-conotoxin
CC PVIIA analogue of the invention.
XX
SQ Sequence 27 AA:

Query Match 92.1%; Score 129; DB 22; Length 27;
Best Local Similarity 81.5%; Pred. No. 5.4e-09;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSXCNXKXCV 27
|||
DB 1 CRXNQKCFQHLDDCCSRKCNARFNKCV 27

RESULT 3

AAU10199
ID AAU10199 standard; peptide: 27 AA.

AC AAU10199;

DT 16-JAN-2002 (first entry)

DE Snail Kappa-conotoxin PVIIA analogue K19A.

KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;

KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischemia;

KW cerebral ischemia; ocular ischemia; asthma; K19A.

OS Conus purpurascens.

OS Synthetic.

FT Key Location/Qualifiers

FT Modified-site 4 /note= "Hydroxyproline"

FT Modified-site 27 /note= "The C-terminus is either a carboxyl group
or an amide group"

PN WO200121648-A1.

PD 29-MAR-2001.

PF 21-SEP-2000; 2000WO-US25827.

PR 22-SEP-1999; 99US-155135P.

PR 20-JUL-2000; 2000US-0219438.

PA (COGN-) COGNETIX INC.

PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
XX
DR WPI: 2001-648090/74.

PT Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma
PT comprises activating a KATP channel by administering to an individual a

PT kappa-conotoxin PVIIA peptide -
XX
XX Claim 1; Page 27; 46pp; English.
XX
CC The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA
CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
CC active salt. The conotoxins are used for treating disorders associated
CC with radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin
CC PVIIA analogue of the invention.
XX
SQ Sequence 27 AA;
Query Match 92.1%; Score 129; DB 22; Length 27;
Best Local Similarity 81.5%; Pred. No. 5.4e-09;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CRXNKCFOHLDCCSXCNXNXCVCV 27
1 CRXNKCFOHLDCCSRACNRFNKCVCV 27
Db
RESULT 4
AAU10202
ID AAU10202 standard; peptide; 27 AA.
XX
AC AAU10202;
XX
DT 16-JAN-2002 (first entry)
XX
DE Snail Kappa-conotoxin PVIIA analogue K25A.
XX
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antisthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; K25A.
XX
OS Conus purpurascens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 4 /note= "Hydroxyproline"
FT Modified-site 27 /note= "The C-terminus is either a carboxyl group
FT or an amide group"
XX
XX WO200121648-A1.
XX
XX 29-MAR-2001.
XX
XX 21-SEP-2000; 2000WO-US25827.
XX
XX 22-SEP-1999; 99US-155135P.
XX 20-JUL-2000; 2000US-0219438.
XX
XX (COGN-) COGNETIX INC.
XX
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
XX
XX WPI; 2001-648090/74.
XX
XX
XX Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma
PT comprises activating a KATP channel by administering to an individual a
PT kappa-conotoxin PVIIA peptide -
XX
XX Claim 1; Page 27; 46pp; English.
XX
XX The invention relates to treating disorders associated with radical

CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA
CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
CC active salt. The conotoxins are used for treating disorders associated
CC with radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin
CC PVIIA analogue of the invention.
XX
SQ Sequence 27 AA;
Query Match 92.1%; Score 129; DB 22; Length 27;
Best Local Similarity 81.5%; Pred. No. 5.4e-09;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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1 CRXNKCFOHLDCCSRACNRFNKCVCV 27
Db
RESULT 5
AAU10218
ID AAU10218 standard; peptide; 27 AA.
XX
AC AAU10218;
XX
DT 16-JAN-2002 (first entry)
XX
DE Snail Kappa-conotoxin PVIIA analogue 04A.
XX
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antisthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; 04A.
XX
OS Conus purpurascens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 4 /note= "Hydroxyproline"
FT Modified-site 27 /note= "The C-terminus is either a carboxyl group
FT or an amide group"
XX
XX WO200121648-A1.
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XX 29-MAR-2001.
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XX 21-SEP-2000; 2000WO-US25827.
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XX 22-SEP-1999; 99US-155135P.
XX 20-JUL-2000; 2000US-0219438.
XX
XX (COGN-) COGNETIX INC.
XX
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
XX
XX WPI; 2001-648090/74.
XX
XX
XX Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma
PT comprises activating a KATP channel by administering to an individual a
PT kappa-conotoxin PVIIA peptide -
XX
XX Claim 1; Page 28; 46pp; English.
XX
XX The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA
CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
CC active salt. The conotoxins are used for treating disorders associated
CC with radical depolarisation of excitable membrane by activating a KATP

CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin
 CC PVIIA analogue of the invention.

XX
 SQ Sequence 27 AA;

Query Match 92.1%; Score 129; DB 22; Length 27;
 Best Local Similarity 77.8%; Pred. No. 5.4e-09;
 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 CRINQKCFQHLDDCCSXKCNXNCV 27
 ||| ||||| ||||| ||| |||
 Db 1 CRINQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 6
 AAW35723 standard; peptide; 27 AA.

XX AAW35723;

XX 03-APR-1998 (first entry)

XX Kappa-conotoxin PVIIA.

KW Kappa-conotoxin PVIIA; potassium channel; neurotransmitter release;
 KM cone snail; venom; goldfish; delta-conotoxin PVIIA; disulphide.

XX Conus purpurascens.

XX Key Location/Qualifiers

FT Modified-site 4 /note= "optionally 4-trans-hydroxyproline,
 FT hydroxyproline or proline"

FT Disulphide-bond 1..16 /note= "disulphide bond"

FT Disulphide-bond 8..20 /note= "disulphide bond"

FT Disulphide-bond 15..26 /note= "disulphide bond"

XX W09734925-A1.

XX 25-SEP-1997.

XX 14-MAR-1997; 97MO-US03483.

XX 18-MAR-1996; 96US-0619936.

XX (UTAH) UNIV UTAH RES FOUND.

XX Grilley MM, Olivera BM, Shon K, Terlau H;

XX WPI; 1997-480162/44.

XX New kappa-conotoxin peptides - which target potassium channels and
 PT can be used to augment neurotransmitter release in e.g. autoimmune
 PT diseases.

XX Claim 1; Page 23; 29pp; English.

XX The present sequence represents a new kappa-conotoxin PVIIA which
 CC targets potassium channels and can be used to augment neurotransmitter
 CC release in pathological situations such as autoimmune diseases, e.g.
 CC Alzheimer's disease, Lambert-Eaton syndrome or myasthenia gravis.
 CC This peptide together with delta-conotoxin PVIIA act synergistically to
 CC rapidly immobilize fish which are injected with the two peptides.
 CC Injection of kappa-conotoxin PVIIA alone results in different symptoms
 CC with an injected fish becoming hyperactive and then contracting and
 CC suddenly extending all major fins. This "fin-popping" occurs repeatedly
 CC resulting in a series of jerky movements, but injection of only
 CC kappa-conotoxin PVIIA does not immobilize or kill the fish.

SQ Sequence 27 AA;

Query Match 90.7%; Score 127; DB 18; Length 27;
 Best Local Similarity 77.8%; Pred. No. 9.4e-09;
 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 CRINQKCFQHLDDCCSXKCNXNCV 27
 ||| ||||| ||||| ||| |||
 Db 1 CRINQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 7
 AAU10203 standard; peptide; 27 AA.

XX AAU10203;

XX 16-JAN-2002 (first entry)

XX Snail Kappa-conotoxin PVIIA analogue R2K.

XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;

KW cardioactive; antihypertensive; KATP channel activation; cardiac ischaemia;
 KM cerebral ischaemia; ocular ischaemia; asthma; R2K.

XX Conus purpurascens.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 4 /note= "Hydroxyproline"

FT Modified-site 27 /note= "The C-terminus is either a carboxyl group
 FT or an amide group"

XX W0200121648-A1.

XX 29-MAR-2001.

XX 21-SEP-2000; 2000MO-US25827.

XX 22-SEP-1999; 99US-155135P.

XX 20-JUL-2000; 2000US-0219438.

XX (COGN-) COGNETIX INC.

XX Corneli-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;

XX Jones KR;

XX WPI; 2001-648090/74.

XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma
 PT comprises activating a KATP channel by administering to an individual a
 PT kappa-conotoxin PVIIA peptide -

XX Claim 1; Page 27; 46pp; English.

XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA
 CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
 CC active salt. The conotoxins are used for treating disorders associated
 CC with radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin
 CC PVIIA analogue of the invention.

XX Sequence 27 AA;

Query Match 89.3%; Score 125; DB 22; Length 27;
 Best Local Similarity 77.8%; Pred. No. 1.6e-08;
 Matches 21; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 CRINXNCKFQHLDDCCSXKCNXXNKCVCV 27
 ID 1 CRINXNCKFQHLDDCCSXKCNXXNKCVCV 27

RESULT 8
 AAU10206

ID AAU10206 standard; peptide; 27 AA.

AC AAU10206;

DT 16-JAN-2002 (first entry)

DE Snail Kappa-conotoxin PVIIA analogue F9Y.

XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;

KM cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;

OS cerebral ischaemia; ocular ischaemia; asthma; F9Y.

OS Conus purpurascens.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 4

FT /note= "Hydroxyproline"

FT Modified-site 27

FT /note= "The C-terminus is either a carboxyl group or an amide group"

XX W0200121648-A1.

XX 29-MAR-2001.

XX 21-SEP-2000; 2000WO-US25827.

XX 22-SEP-1999; 99US-155135P.

XX 20-JUL-2000; 2000US-0219438.

XX (COGN-) COGNETIX INC.

XX Corneli-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;

XX Jones RR;

XX WPI; 2001-648090/74.

XX Treating disorders associated with radical depolarization of excitable

XX membrane e.g. cardiac, cerebral and ocular ischaemia and asthma

XX comprises activating a KATP channel by administering to an individual a

XX kappa-conotoxin PVIIA peptide -

XX Claim 1; Page 28; 46pp; English.

XX The invention relates to treating disorders associated with radical

XX depolarisation of excitable membrane by activating a KATP channel

XX comprising administering to an individual a kappa-conotoxin PVIIA

XX (kappa-PVIIA) peptide or its analogue, derivative or physiologically

XX active salt. The conotoxins are used for treating disorders associated

XX with radical depolarisation of excitable membrane by activating a KATP

XX channel, especially cardiac ischaemia, cerebral ischaemia, ocular

XX ischaemia and asthma. The present sequence is a kappa-conotoxin

XX PVIIA analogue of the invention.

SO Sequence 27 AA;

Query Match 89.3%; Score 125; DB 22; Length 27;

Best Local Similarity 77.8%; Pred. No. 1.6e-08;

Matches 21; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 CRINXNCKFQHLDDCCSXKCNXXNKCVCV 27

Db 1 CRINXNCKFQHLDDCCSXKCNXXNKCVCV 27

RESULT 9
 AAU10212
 ID AAU10212 standard; peptide; 27 AA.

AC AAU10212;

DT 16-JAN-2002 (first entry)

DE Snail Kappa-conotoxin PVIIA analogue S17A.

XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;

KM cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;

OS cerebral ischaemia; ocular ischaemia; asthma; S17A.

OS Conus purpurascens.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 4

FT /note= "Hydroxyproline"

FT Modified-site 27

FT /note= "The C-terminus is either a carboxyl group or an amide group"

XX W0200121648-A1.

XX 29-MAR-2001.

XX 21-SEP-2000; 2000WO-US25827.

XX 22-SEP-1999; 99US-155135P.

XX 20-JUL-2000; 2000US-0219438.

XX (COGN-) COGNETIX INC.

XX Corneli-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;

XX Jones RR;

XX WPI; 2001-648090/74.

XX Treating disorders associated with radical depolarisation of excitable

XX membrane e.g. cardiac, cerebral and ocular ischaemia and asthma

XX comprises activating a KATP channel by administering to an individual a

XX kappa-conotoxin PVIIA peptide -

XX Claim 1; Page 28; 46pp; English.

XX The invention relates to treating disorders associated with radical

XX depolarisation of excitable membrane by activating a KATP channel

XX comprising administering to an individual a kappa-conotoxin PVIIA

XX (kappa-PVIIA) peptide or its analogue, derivative or physiologically

XX active salt. The conotoxins are used for treating disorders associated

XX with radical depolarisation of excitable membrane by activating a KATP

XX channel, especially cardiac ischaemia, cerebral ischaemia, ocular

XX ischaemia and asthma. The present sequence is a kappa-conotoxin

XX PVIIA analogue of the invention.

SO Sequence 27 AA;

Query Match 89.3%; Score 125; DB 22; Length 27;

Best Local Similarity 77.8%; Pred. No. 1.6e-08;

Matches 21; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 CRINXNCKFQHLDDCCSXKCNXXNKCVCV 27

Db 1 CRINXNCKFQHLDDCCSXKCNXXNKCVCV 27

RESULT 10
 AAU10207
 ID AAU10207 standard; peptide; 27 AA.

```

AC AAU10207;
XX
XX 16-JAN-2002 (first entry)
XX
XX Snail Kappa-conotoxin PVIIA analogue R2Q.
DE
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KM cardioactive; antisthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; R2Q.
XX
XX Conus purpurascens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 4
FT Modified-site /note="Hydroxyproline"
FT Modified-site 27
FT /note="The C-terminus is either a carboxyl group
FT or an amide group"
XX
XX WO200121648-A1.
XX
XX 29-MAR-2001.
XX
XX 21-SEP-2000; 2000WO-US25827.
XX
XX 22-SEP-1999; 99US-155135P.
XX 20-JUL-2000; 2000US-0219438.
XX
XX (COGN-) COGNETIX INC.
XX
XX Cornelli-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
XX Jones RR.
XX
XX WPI; 2001-648090/74.
XX
XX Treating disorders associated with radical depolarization of excitable
XX membrane e.g. cardiac, cerebral and ocular ischaemia and asthma
XX comprises activating a KATP channel by administering to an individual a
XX kappa-conotoxin PVIIA peptide -
XX
XX Claim 1; Page 28; 46pp; English.
XX
XX The invention relates to treating disorders associated with radical
XX depolarisation of excitable membrane by activating a KATP channel
XX comprising administering to an individual a kappa-conotoxin PVIIA
XX (kappa-PVIIA) peptide or its analogue, derivative or physiologically
XX active salt. The conotoxins are used for treating disorders associated
XX with radical depolarisation of excitable membrane by activating a KATP
XX channel, especially cardiac ischaemia, cerebral ischaemia, ocular
XX ischaemia and asthma. The present sequence is a kappa-conotoxin
XX PVIIA analogue of the invention.
XX
XX Sequence 27 AA;
XX
XX Query Match 88.6%; Score 124; DB 22; Length 27;
XX Best Local Similarity 77.8%; Pred. No. 2.1e-08;
XX Matches 21; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 CRXNOKCFQHLDDCCSXCNXXNXC 27
XX I:||||| 11 11
XX 1 CRXNOKCFQHLDDCCSRKCNRFNKC 27
XX
XX RESULT 11
XX AAU10217
XX ID AAU10217 standard; peptide; 27 AA.
XX
XX AC AAU10217;
XX
XX 16-JAN-2002 (first entry)
XX
XX Snail Kappa-conotoxin PVIIA analogue V27A.
XX

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XX
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KM cardioactive; antisthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; V27A.
XX
XX Conus purpurascens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 4
FT Modified-site /note="Hydroxyproline"
FT Modified-site 27
FT /note="The C-terminus is either a carboxyl group
FT or an amide group"
XX
XX WO200121648-A1.
XX
XX 29-MAR-2001.
XX
XX 21-SEP-2000; 2000WO-US25827.
XX
XX 22-SEP-1999; 99US-155135P.
XX 20-JUL-2000; 2000US-0219438.
XX
XX (COGN-) COGNETIX INC.
XX
XX Cornelli-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
XX Jones RR.
XX
XX WPI; 2001-648090/74.
XX
XX Treating disorders associated with radical depolarization of excitable
XX membrane e.g. cardiac, cerebral and ocular ischaemia and asthma
XX comprises activating a KATP channel by administering to an individual a
XX kappa-conotoxin PVIIA peptide -
XX
XX Claim 1; Page 28; 46pp; English.
XX
XX The invention relates to treating disorders associated with radical
XX depolarisation of excitable membrane by activating a KATP channel
XX comprising administering to an individual a kappa-conotoxin PVIIA
XX (kappa-PVIIA) peptide or its analogue, derivative or physiologically
XX active salt. The conotoxins are used for treating disorders associated
XX with radical depolarisation of excitable membrane by activating a KATP
XX channel, especially cardiac ischaemia, cerebral ischaemia, ocular
XX ischaemia and asthma. The present sequence is a kappa-conotoxin
XX PVIIA analogue of the invention.
XX
XX Sequence 27 AA;
XX
XX Query Match 88.6%; Score 124; DB 22; Length 27;
XX Best Local Similarity 80.8%; Pred. No. 2.1e-08;
XX Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 CRXNOKCFQHLDDCCSXCNXXNXC 26
XX I:||||| 11 11
XX 1 CRXNOKCFQHLDDCCSRKCNRFNKC 26
XX
XX RESULT 12
XX AAU10198
XX ID AAU10198 standard; peptide; 27 AA.
XX
XX AC AAU10198;
XX
XX 16-JAN-2002 (first entry)
XX
XX Snail Kappa-conotoxin PVIIA analogue I3A.
XX
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KM cardioactive; antisthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; I3A.
XX

```

OS Conus purpurascens.
 OS Synthetic.
 XX
 FT Key
 FT Modified-site 4 Location/Qualifiers
 FT Modified-site 27 /note="Hydroxyproline"
 FT Modified-site 27 /note="The C-terminus is either a carboxyl group or an amide group"
 FT
 XX
 PN W0200121648-A1.
 XX
 XX
 PD 29-MAR-2001.
 XX
 PF 21-SEP-2000; 2000WO-US25827.
 XX
 PR 22-SEP-1999; 99US-155135P.
 PR 20-JUL-2000; 2000US-0219438.
 XX
 PA (COGN-) COGNETIX INC.
 XX
 PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 XX
 DR WPI; 2001-648090/74.
 XX
 XX Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma
 PT comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide -
 PT
 PS Claim 1; Page 27; 46pp; English.
 XX
 CC The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischemia, cerebral ischemia, ocular ischemia and asthma. The present sequence is a kappa-conotoxin CC PVIIA analogue of the invention.
 CC
 XX
 SQ Sequence 27 AA;
 Query Match 87.9%; Score 123; DB 22; Length 27;
 Best Local Similarity 77.8%; Pred. No. 2.8e-08;
 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CRXNOKCFQHLDDCCSXCNXXNXCXV 27
 DB 1 CRAXNOKCFQHLDDCCSRKCNRFNKCXV 27
 RESULT 13
 AAU10214
 ID AAU10214 standard; peptide; 27 AA.
 XX
 AC AAU10214;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE Snail Kappa-conotoxin PVIIA analogue L12A.
 XX
 KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antisthmatic; KATP channel activation; cardiac ischemia; cerebral ischemia; ocular ischemia; asthma; L12A.
 KW
 XX Conus purpurascens.
 OS Synthetic.
 OS
 XX Key
 FT Modified-site 4 Location/Qualifiers

FT Modified-site 27 /note="Hydroxyproline"
 FT Modified-site 27 /note="The C-terminus is either a carboxyl group or an amide group"
 FT
 XX
 PN W0200121648-A1.
 XX
 XX
 PD 29-MAR-2001.
 XX
 PF 21-SEP-2000; 2000WO-US25827.
 XX
 PR 22-SEP-1999; 99US-155135P.
 PR 20-JUL-2000; 2000US-0219438.
 XX
 PA (COGN-) COGNETIX INC.
 XX
 PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 XX
 DR WPI; 2001-648090/74.
 XX
 XX Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma
 PT comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide -
 PT
 PS Claim 1; Page 28; 46pp; English.
 XX
 CC The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischemia, cerebral ischemia, ocular ischemia and asthma. The present sequence is a kappa-conotoxin CC PVIIA analogue of the invention.
 CC
 XX
 SQ Sequence 27 AA;
 Query Match 87.9%; Score 123; DB 22; Length 27;
 Best Local Similarity 77.8%; Pred. No. 2.8e-08;
 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CRXNOKCFQHLDDCCSXCNXXNXCXV 27
 DB 1 CRXNOKCFQHLDDCCSRKCNRFNKCXV 27
 RESULT 14
 AAU10200
 ID AAU10200 standard; peptide; 27 AA.
 XX
 AC AAU10200;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE Snail Kappa-conotoxin PVIIA analogue R2A.
 XX
 KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antisthmatic; KATP channel activation; cardiac ischemia; cerebral ischemia; ocular ischemia; asthma; R2A.
 KW
 XX Conus purpurascens.
 OS Synthetic.
 OS
 XX Key
 FT Modified-site 4 Location/Qualifiers
 FT Modified-site 27 /note="Hydroxyproline"
 FT Modified-site 27 /note="The C-terminus is either a carboxyl group or an amide group"

PN WO200121648-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 21-SEP-2000; 2000WO-US25827.
 XX
 PR 22-SEP-1999; 99US-155135P.
 PR 20-JUL-2000; 2000US-0219438.
 XX
 PA (COGN-) COGNETIX INC.
 XX
 PI Corneli-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 DR WPI; 2001-648090/74.
 XX
 PT Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma
 PT comprises activating a KATP channel by administering to an individual a
 PT kappa-conotoxin PVIIA peptide -
 XX
 PS Claim 1; Page 27; 46pp; English.
 CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA
 CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
 CC active salt. The conotoxins are used for treating disorders associated
 CC with radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin
 CC PVIIA analogue of the invention.
 CC
 SQ Sequence 27 AA:
 87.1%; Score 122; DB 22; Length 27;
 Query Match Best Local Similarity 77.8%; Pred. No. 3.7e-08;
 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CRXNKCFOHLDCCSXNCXNKCXCV 27
 Db 1 CAIXNKCFOHLDCCSRKCNRFNKCXCV 27
 RESULT 15
 AAU10204
 ID AAU10204 standard; peptide; 27 AA.
 XX
 AC AAU10204;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE Small kappa-conotoxin PVIIA analogue K7A.
 XX
 KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antisthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; K7A.
 XX
 OS Conus purpurascens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4
 FT Modified-site 27 /note- "Hydroxyproline"
 FT Modified-site 27 /note- "The C-terminus is either a carboxyl group
 FT or an amide group"
 XX
 PN WO200121648-A1.
 XX
 PD 29-MAR-2001.
 PD
 PF 21-SEP-2000; 2000WO-US25827.

XX
 PR 22-SEP-1999; 99US-155135P.
 PR 20-JUL-2000; 2000US-0219438.
 XX
 PA (COGN-) COGNETIX INC.
 XX
 PI Corneli-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 DR WPI; 2001-648090/74.
 XX
 PT Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma
 PT comprises activating a KATP channel by administering to an individual a
 PT kappa-conotoxin PVIIA peptide -
 XX
 PS Claim 1; Page 28; 46pp; English.
 CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA
 CC (kappa-PVIIA) peptide or its analogue, derivative or physiologically
 CC active salt. The conotoxins are used for treating disorders associated
 CC with radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin
 CC PVIIA analogue of the invention.
 CC
 SQ Sequence 27 AA:
 87.1%; Score 122; DB 22; Length 27;
 Query Match Best Local Similarity 77.8%; Pred. No. 3.7e-08;
 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CRXNKCFOHLDCCSXNCXNKCXCV 27
 Db 1 CRXNKCFOHLDCCSRKCNRFNKCXCV 27
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 Job time : 36 secs

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OM protein - protein search, using sw model

Run on: January 14, 2003, 18:27:36 ; Search time 14 Seconds

(without alignments)
56,744 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 6: /cg02_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	128	91.4	27	1	US-08-619-936-1
2	64	45.7	26	1	US-07-789-913-19
3	64	45.7	26	1	US-08-049-794-19
4	64	45.7	26	1	US-08-496-847-19
5	64	45.7	26	2	US-08-742-774-19
6	64	45.7	26	2	US-08-675-354-19
7	64	45.7	26	2	US-08-965-918-19
8	64	45.7	26	2	US-09-138-439-19
9	64	45.7	26	3	US-08-613-400A-19
10	64	45.7	26	3	US-09-298-017-19
11	64	45.7	26	4	US-09-392-979A-19
12	64	42.9	26	1	US-07-789-913-8
13	64	42.9	26	1	US-08-049-794-8
14	64	42.9	26	1	US-08-496-847-8
15	64	42.9	26	2	US-08-742-774-8
16	64	42.9	26	2	US-08-675-354-8
17	64	42.9	26	2	US-08-965-918-8
18	64	42.9	26	2	US-09-138-439-8
19	64	42.9	26	3	US-08-613-400A-8
20	64	42.9	26	3	US-09-298-017-8
21	64	42.9	26	4	US-09-392-979A-8
22	56	40.0	2523	1	US-08-185-432-18
23	56	40.0	2523	4	US-08-899-232-3
24	55	39.3	2703	4	US-08-185-432-19
25	55	39.3	2703	4	US-08-899-232-4
26	52	37.1	1964	4	US-09-467-997-1
27	52	37.1	2556	1	US-08-185-432-17

28	52	37.1	2556	1	US-08-083-550A-20	Sequence 20, Appl
29	52	37.1	2556	3	US-08-532-384-20	Sequence 20, Appl
30	52	37.1	2556	4	US-08-899-232-2	Sequence 21, Appl
31	50	35.7	26	1	US-08-049-794-21	Sequence 21, Appl
32	50	35.7	26	1	US-08-049-794-29	Sequence 21, Appl
33	50	35.7	26	1	US-08-496-847-21	Sequence 21, Appl
34	50	35.7	26	1	US-08-496-847-29	Sequence 21, Appl
35	50	35.7	26	2	US-08-742-774-21	Sequence 21, Appl
36	50	35.7	26	2	US-08-742-774-29	Sequence 21, Appl
37	50	35.7	26	2	US-08-675-354-21	Sequence 21, Appl
38	50	35.7	26	2	US-08-675-354-29	Sequence 21, Appl
39	50	35.7	26	2	US-08-965-918-21	Sequence 21, Appl
40	50	35.7	26	2	US-08-965-918-29	Sequence 21, Appl
41	50	35.7	26	2	US-09-138-439-21	Sequence 21, Appl
42	50	35.7	26	2	US-09-138-439-29	Sequence 21, Appl
43	50	35.7	26	3	US-08-613-400A-21	Sequence 21, Appl
44	50	35.7	26	3	US-08-613-400A-29	Sequence 21, Appl
45	50	35.7	26	3	US-09-298-017-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-619-936-1
Sequence 1, Application US/08619936
Patent No. 5672682
GENERAL INFORMATION:
APPLICANT: Terlau, Heinrich
APPLICANT: Shon, Ki-Uoon
APPLICANT: Grille, Michelle
APPLICANT: Oliveira, Baldomero M.
TITLE OF INVENTION: Conotoxin Peptide PVIIA
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,936
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 24260-107674-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus purpurascens
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product="4Hyp"
OTHER INFORMATION: /note="Amino acid 4 may be 4-trans-hydroxyproline."

GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohl, Kishorendra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristilpati, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-08-496-847-19
Query Match 45.7%; Score 64; DB 1; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.059;
Matches 9; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
OY 1 CRXNQKCFQHLDDCCSXCNXXNXC 26
DB 1 CKLKGSCSRIMWDCSCSGSGRSGKC 26
RESULT 5
US-08-742-774-19
Sequence 19, Application US/08/42774
Patent No. 5824645
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US/08/049,794

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US/07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-08-742-774-19
Query Match 45.7%; Score 64; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.059;
Matches 9; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
OY 1 CRXNQKCFQHLDDCCSXCNXXNXC 26
DB 1 CKLKGSCSRIMWDCSCSGSGRSGKC 26
RESULT 6
US-08-675-354-19
Sequence 19, Application US/08/675354
Patent No. 5859186
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US/08/049,794

;
HYPOTHETICAL: NO

QY 1 CR1XN0KCF0HLDDCCSXXCNNXXNC 26

Db 1 CKLKGSCLMYDCCSGSCGRSGC 26

RESULT 9
US-08-613-400A-19
Sequence 19, Application US/08613400A
Patent No. 6054429
GENERAL INFORMATION:
APPLICANT: Bowersox, S. Scott
APPLICANT: Gadbois, Theresa
APPLICANT: Pettus, Mark, R.
APPLICANT: Luther, Robert, R.
TITLE OF INVENTION: IMPROVED EPIDURAL
TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0019
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-08-613-400A-19
Query Match 45.7%; Score 64; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.059;
Matches 9; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
OY 1 CRXNKCFOHLDCCSXCNXXNC 26
1 CRLKGSCSRIMYDCCSGSGRSGKC 26
Db 1 CRLKGSCSRIMYDCCSGSGRSGKC 26
RESULT 10
US-09-298-017-19
Sequence 19, Application US/09298017
Patent No. 6087091
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILVANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPiate ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,017
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-09-298-017-19
Query Match 45.7%; Score 64; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.059;
Matches 9; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
OY 1 CRXNKCFOHLDCCSXCNXXNC 26
1 CRLKGSCSRIMYDCCSGSGRSGKC 26
Db 1 CRLKGSCSRIMYDCCSGSGRSGKC 26
RESULT 11
US-09-392-979A-19
Sequence 19, Application US/09392979A
Patent No. 6136786
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILVANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPiate ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-09-392-979A-19

Query Match 45.7%; Score 64; DB 4; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.059;
Matches 9; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

OY 1 CRXNOKCFQHLDDCCSXCNXNXC 26
DB 1 CKLKGSCSRKTSYDCCSGSGCRSGKC 26

RESULT 12
US-07-789-913-8
Sequence 8, Application US/07789913
Patent No. 5559095
GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Fox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Blitner, Robert S.
APPLICANT: Yamashiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing
TITLE OF INVENTION: Ischemia-Related Neuronal Damage
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: AMINO ACID
TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-183
US-07-789-913-8

Query Match 42.9%; Score 60; DB 1; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.18;
Matches 9; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

OY 1 CRXNOKCFQHLDDCCSXCNXNXC 26
DB 1 CKLKGSCSRKTSYDCCSGSGCRSGKC 26

RESULT 13
US-08-049-794-8
Sequence 8, Application US/08049794
Patent No. 5587454
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L.
APPLICANT: MILJANICH, GEORGE P.
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SV1B/SNX-183, FIGURE 1
US-08-049-794-8

APPLICANT: SINGH, TEJINDER

Search completed: January 14, 2003, 18:29:47
Job time : 15 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 18:28:16 : Search time 11 Seconds
(without alignments)
47.621 Million cell updates/sec

Title: US-09-666-837b-1-COPY
Perfect score: 140
Sequence: 1 CRXNCKCFQHDCCSXNXXNXCXV 27

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications-AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/2/pubppaa/PCIT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubppaa/PCITUS_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58.5	41.8	35	10	US-09-894-882-120
2	56.5	40.4	35	10	US-09-894-882-413
3	56.5	40.4	36	10	US-09-894-882-168
4	56.5	40.4	36	10	US-09-894-882-210
5	56.5	40.4	36	10	US-09-894-882-404
6	56.5	40.4	70	10	US-09-894-882-209
7	56.5	40.4	71	10	US-09-894-882-119
8	55.5	39.6	36	10	US-09-894-882-201
9	55.5	39.6	36	10	US-09-894-882-401
10	55.5	39.6	42	10	US-09-894-882-306
11	55.5	39.6	42	10	US-09-894-882-452
12	55.5	39.6	70	10	US-09-894-882-200
13	55.5	39.6	75	10	US-09-894-882-305
14	54.5	38.9	36	10	US-09-894-882-369
15	54.5	38.9	73	10	US-09-894-882-167
16	52.5	37.1	35	10	US-09-894-882-75
17	52	37.1	2444	10	US-09-944-849-2
18	51.5	36.8	35	10	US-09-894-882-159
19	51.5	36.8	36	10	US-09-894-882-156

20	51.5	36.8	36	10	US-09-894-882-174	Sequence 177, App
21	51.5	36.8	36	10	US-09-894-882-177	Sequence 177, App
22	51.5	36.8	36	10	US-09-894-882-403	Sequence 403, App
23	51.5	36.8	36	10	US-09-894-882-426	Sequence 226, App
24	51.5	36.8	70	10	US-09-894-882-206	Sequence 206, App
25	50.5	36.1	35	10	US-09-894-882-433	Sequence 433, App
26	50.5	36.1	36	10	US-09-894-882-216	Sequence 216, App
27	50.5	36.1	36	10	US-09-894-882-406	Sequence 406, App
28	50.5	36.1	42	10	US-09-894-882-309	Sequence 309, App
29	50.5	36.1	42	10	US-09-894-882-312	Sequence 312, App
30	50.5	36.1	42	10	US-09-894-882-449	Sequence 449, App
31	50.5	36.1	42	10	US-09-894-882-450	Sequence 450, App
32	50.5	36.1	70	10	US-09-894-882-215	Sequence 215, App
33	50.5	36.1	71	10	US-09-894-882-74	Sequence 74, App
34	50.5	36.1	75	10	US-09-894-882-308	Sequence 308, App
35	50.5	36.1	75	10	US-09-894-882-311	Sequence 311, App
36	50.5	36.1	76	9	US-09-749-637A-207	Sequence 311, App
37	50	35.7	176	9	US-10-024-599-4	Sequence 4, App
38	49.5	35.4	29	9	US-09-749-637A-208	Sequence 208, App
39	49.5	35.4	35	10	US-09-894-882-366	Sequence 366, App
40	49.5	35.4	36	10	US-09-894-882-165	Sequence 165, App
41	49.5	35.4	36	10	US-09-894-882-207	Sequence 207, App
42	49.5	35.4	36	10	US-09-894-882-365	Sequence 365, App
43	49.5	35.4	36	10	US-09-894-882-368	Sequence 368, App
44	49.5	35.4	36	10	US-09-894-882-371	Sequence 371, App
45	49.5	35.4	36	10	US-09-894-882-372	Sequence 372, App

ALIGNMENTS

RESULT 1
US-09-894-882-120
Sequence 120, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Oliviera, Baldemero M.
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894, 882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 120
LENGTH: 35
TYPE: PRT
ORGANISM: Conus magus
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(35)
OTHER INFORMATION: Xaa at residue 33 is Pro or hydroxy-Pro; Xaa at residue 25 is
OTHER INFORMATION: or gamma-carboxy-Glu; Xaa at residue 18 is Trp or bromo-Tr
US-09-894-882-120


```
; OTHER INFORMATION: Tyr, 125I-Tyr, mono-Iodo-Tyr, di-Iodo-Tyr, O-sulpho-Tyr or O-pho
; OTHER INFORMATION: spho-Tyr
US-09-894-882-210

Query Match          40.4%; Score 56.5; DB 10; Length 36;
Best Local Similarity 44.4%; Pred. No. 0.14;
Matches 12; Conservative 1; Mismatches 13; Indels 1; Gaps 1;

OY 1 CRXNOKCFQHLDDCCSXKXCNXXKCV 27
    || | |||: | | | |
Db 5 CFNAGVKCDNH-SDCCADTCCYDNTCV 30

RESULT 5
US-09-894-882-404
; Sequence 404, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 404
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus lynceus
US-09-894-882-404

Query Match          40.4%; Score 56.5; DB 10; Length 36;
Best Local Similarity 40.7%; Pred. No. 0.14;
Matches 11; Conservative 1; Mismatches 14; Indels 1; Gaps 1;

OY 1 CRXNOKCFQHLDDCCSXKXCNXXKCV 27
    || | |||: | | | |
Db 5 CFNAGVKCDNH-SDCCADTCCYDNTCV 30

RESULT 6
US-09-894-882-209
; Sequence 209, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
```

```
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 209
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Conus lynceus
US-09-894-882-209

Query Match          40.4%; Score 56.5; DB 10; Length 70;
Best Local Similarity 37.0%; Pred. No. 0.26;
Matches 10; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

OY 1 CRXNOKCFQHLDDCCSXKXCNXXKCV 27
    || | |||: | | | |
Db 39 CFNAGVKCDNH-SDCCADTCCYDNTCV 64

RESULT 7
US-09-894-882-119
; Sequence 119, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 119
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Conus magus
US-09-894-882-119

Query Match          40.4%; Score 56.5; DB 10; Length 71;
Best Local Similarity 37.0%; Pred. No. 0.26;
Matches 10; Conservative 2; Mismatches 14; Indels 1; Gaps 1;
```

OY 1 CRXNOKCFQHLDDCCSXKXNXXCV 27
DB 39 CSLGQRCGDH-SDCCWDMCASCSEMCV 64

RESULT 8
US-09-894-882-201
Sequence 201, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 201
LENGTH: 36
TYPE: PRT
ORGANISM: Conus lynceus
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(36)
OTHER INFORMATION: Xaa at residue 20 is Glu or gamma-carboxy-Glu; Xaa at residues 2
OTHER INFORMATION: and 4 is Trp or bromo-Trp; Xaa at residue 25 is Tyr, 125I-Tyr, mo
OTHER INFORMATION: no-Iodo-Tyr, di-Iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
US-09-894-882-201

Query Match 39.6%; Score 55.5; DB 10; Length 36;
Best Local Similarity 44.4%; Pred. No. 0.2;
Matches 12; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

OY 1 CRXNOKCFQHLDDCCSXKXNXXCV 27
DB 5 CFNAGVKCDNH-SDCCXDTCCXDNTCV 30

RESULT 9
US-09-894-882-401
Sequence 401, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins

FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 401
LENGTH: 36
TYPE: PRT
ORGANISM: Conus lynceus
US-09-894-882-401

Query Match 39.6%; Score 55.5; DB 10; Length 36;
Best Local Similarity 40.7%; Pred. No. 0.2;
Matches 11; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

OY 1 CRXNOKCFQHLDDCCSXKXNXXCV 27
DB 5 CFNAGVKCDNH-SDCCEDTCCYDNTCV 30

RESULT 10
US-09-894-882-306
Sequence 306, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 306
LENGTH: 42
TYPE: PRT
ORGANISM: Conus aulicus
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(42)
OTHER INFORMATION: Xaa at residue 36 is Pro or hydroxy-Pro; Xaa at residue 12 is
OTHER INFORMATION: or gamma-carboxy-Glu; Xaa at residues 3 and 8 is Trp or bromo-
OTHER INFORMATION: p; Xaa at residue 34 is Tyr, 125I-Tyr, mono-Iodo-Tyr, di-Iodo-
OTHER INFORMATION: O-sulpho-Tyr or O-phospho-Ty
US-09-894-882-306

Query Match 39.6%; Score 55.5; DB 10; Length 42;
Best Local Similarity 33.3%; Pred. No. 0.22;
Matches 9; Conservative 3; Mismatches 14; Indels 1; Gaps 1;

OY 1 CRXNOKCFQHLDDCCSXKXNXXNCV 27
DB 6 CSMSGQEC-KHVSDDCGSFCCVGRCL 31

RESULT 11
US-09-894-882-452
Sequence 452, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894, 882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 452
LENGTH: 42
TYPE: PRT
ORGANISM: Conus aulicus
US-09-894-882-452

Query Match 39.6%; Score 55.5; DB 10; Length 42;
Best Local Similarity 33.3%; Pred. No. 0.22;
Matches 9; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

OY 1 CRXNOKCFQHLDDCCSXKXNXXNCV 27
DB 6 CSMSGQEC-KHVSDDCGSFCCVGRCL 31

RESULT 12
US-09-894-882-200
Sequence 200, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238

Query Match 39.6%; Score 55.5; DB 10; Length 70;
Best Local Similarity 40.7%; Pred. No. 0.35;
Matches 11; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

OY 1 CRXNOKCFQHLDDCCSXKXNXXNCV 27
DB 39 CFNAGVKCDNH-SDCEDPFCYDNTCV 64

RESULT 13
US-09-894-882-305
Sequence 305, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894, 882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 305
LENGTH: 75
TYPE: PRT
ORGANISM: Conus aulicus
US-09-894-882-305

Query Match 39.6%; Score 55.5; DB 10; Length 75;
Best Local Similarity 33.3%; Pred. No. 0.37;
Matches 9; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

OY 1 CRXNOKCFQHLDDCCSXKXNXXNCV 27
DB 39 CSMSGQEC-KHVSDDCGSFCCVGRCL 64

RESULT 14
US-09-894-882-369
; Sequence 369, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 369
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-369

Query Match 38.9%; Score 54.5; DB 10; Length 36;
Best Local Similarity 37.0%; Pred. No. 0.26;
Matches 10; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

QY 1 CRXNKCFOHLDCCSXXCNXNKC 27
DB 2 CLSLGRCERH-SDCCGYLCCEFYDKCV 27

RESULT 15
US-09-894-882-167
; Sequence 167, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 167
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-167

Query Match 38.9%; Score 54.5; DB 10; Length 73;
Best Local Similarity 37.0%; Pred. No. 0.49;
Matches 10; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 167
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-167

QY 1 CRXNKCFOHLDCCSXXCNXNKC 27
DB 39 CLSLGRCERH-SDCCGYLCCEFYDKCV 64

Search completed: January 14, 2003, 18:30:04
Job time : 11 secs

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OM protein - protein search, using sw model

Run on: January 14, 2003, 18:27:06 ; Search time 15 Seconds
(without alignments)
173.042 Million cell updates/sec

Title: US-09-666-837b-1-COPY

Perfect score: 140

Sequence: 1 CRINQKCFQHLDDCCSXKXNXXCV 27

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	90.7	27	2	A58997 kappa-conotoxin PV
2	60	42.9	26	2	C44379 omega-conotoxin SV
3	56	40.0	2524	2	A35844 Xorich protein - Af
4	55	39.3	2703	1	A24420 notch protein - fr
5	52	37.1	1964	2	T09059 notch4 - mouse
6	52	37.1	2437	2	S42612 transmembrane prot
7	52	37.1	2555	2	A40043 notch protein homo
8	51	36.4	2531	2	S18188 notch protein homo
9	51	36.4	2531	2	A46019 Notch-1 protein -
10	50	35.7	29	2	JH0699 omega-conotoxin MV
11	50	35.7	354	2	T22274 hypothetical prote
12	50	35.7	1203	2	A48175 Notch B protein
13	50	35.7	2471	2	A48128 cell-fate determin
14	49	35.0	358	2	E86452 protein FEN1B.15 l
15	49	35.0	601	2	T22025 hypothetical prote
16	49	35.0	601	2	D89711 protein F40E10.4 l
17	49	35.0	2318	2	A45306 notch 3 protein -
18	49	35.0	2321	2	S78549 notch3 protein - h
19	49	35.0	2352	2	T30201 Notch homolog prot
20	49	35.0	3623	2	T08618 intrinsic factor-B
21	48.5	34.6	1208	2	T27822 hypothetical prote
22	48	34.3	293	2	B26637 neurogenic repetit
23	48	34.3	1372	2	T25933 hypothetical prote
24	48	34.3	2139	2	A35672 crumbs protein - f
25	48	34.3	2531	2	T30707 notch homolog - se
26	47.5	33.9	53	2	T30499 conotoxin-like pro
27	47.5	33.9	53	2	T10405 conotoxin-like pro
28	47	33.6	25	2	JH0700 omega-conotoxin MV
29	47	33.6	29	2	B43620 omega-conotoxin GV

30	47	33.6	832	2	A31246 neurogenic protein
31	47	33.6	833	2	S19087 gene Delta protein
32	47	33.6	880	2	S00670 neurogenic repetit
33	47	33.6	1064	2	A40136 fibropellin Ia - s
34	47	33.6	1469	2	B36655 silt protein 2 pre
35	47	33.6	1480	2	A36655 conotoxin homolog
36	46.5	33.2	53	2	C72850 omega-conotoxin MV
37	46	32.9	25	2	JH0701 hypothetical prote
38	46	32.9	644	2	S64135 DELTA-like 1 - mou
39	46	32.9	722	2	T48324 EGF repeat transme
40	46	32.9	1687	2	T30176 hypothetical prote
41	45.5	32.5	99	2	T26416 transcription init
42	45.5	32.5	503	2	A58537 omega-conotoxin MV
43	45	32.1	29	2	H64561 invalid gene - Hel
44	45	32.1	138	2	H64561 fibropellin C prec
45	45	32.1	570	2	A48836

ALIGNMENTS

RESULT 1

A58997

kappa-conotoxin PVIIA - cone shell (Conus purpurascens)

N.Alternate names: fin-popping peptide

C.Species: Conus purpurascens (purple cone)

C.Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999

C.Accession: A58997

R.Retlau, H.; Shon, K.J.; Grilley, M.; Stocker, M.; Stuelmer, W.; Olivera, B.M.

Nature 381, 148-151, 1996

A.Title: Strategy for rapid immobilization of prey by a fish-hunting marine snail.

A.Reference number: A58997

A.Accession: A58997

A.Status: preliminary

A.Molecule type: protein

A.Residues: 1-27 <PER>

C.Comment: This conotoxin blocks conductance of the Shaker potassium channel.

C.Keywords: hydroxyproline; neurotoxin; venom

F/4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 90.7%; Score 127; DB 2; Length 27;

Best Local Similarity 77.8%; Pred. No. 6.6e-10;

Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CRINQKCFQHLDDCCSXKXNXXCV 27

DB 1 CRINQKCFQHLDDCCSRKCNFKVCV 27

RESULT 2

C44379

omega-conotoxin SVIIB [validated] - cone shell (Conus striatus)

N.Alternate names: SNK-183

C.Species: Conus striatus (striated cone)

C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Sep-2000

C.Accession: C44379

R.Ramilo, C.A.; Zafraalla, G.C.; Nadaedi, L.; Hammerland, L.G.; Yoshikami, D.; Gray,

Biochemistry 31, 9919-9926, 1992

A.Title: Novel alpha- and omega-conotoxins from Conus striatus venom.

A.Reference number: A44379; MUID:93003172; PMID:1390774

A.Accession: C44379

A.Molecule type: protein

A.Residues: 1-26 <RAM>

A.Cross-references: CAS:143306-19-8

A.Experimental source: venom

A.Note: sequence extracted from NCBI backbone (NCBIP:116002); structure confirmed by

submitted to the Brookhaven Protein Data Bank, August 1996

R.Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.

A.Reference number: A67649; PDB:1MVJ

A.Contents: annotation; conformation by (1)H-NMR, residues 1-26

J. Mol. Biol. 263, 297-310, 1996

A.Title: A consensus structure for omega-conotoxins with different selectivities for

A:Reference number: A58619; MUID:97070382; PMID:8913308
 A:Contents: annotation; conformation by (1)H-NMR
 A:Comment: This omega-conotoxin blocks presynaptic calcium channels.
 C:Superfamily: omega-conotoxin
 C:Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel int
 F:1-16-8-20,15-26/Disulfide bonds: #status predicted
 F:26/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 42.9%; Score 60; DB 2; Length 26;
 Best Local Similarity 34.6%; Pred. No. 0.21;
 Matches 9; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 1 CRXNQCFOHLDCCSXCNXXNCV 26
 Db 1 CKLKGCSCRTSYDCCSGCGSGKC 26

RESULT 3

A35844
 Xotch protein - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 02-Aug-2002
 C:Accession: A35844
 R:Coffman, C.; Harris, W.; Kintner, C.
 Science 249, 1438-1441, 1990
 A:Title: Xotch, the Xenopus homolog of Drosophila notch.
 A:Reference number: A35844; MUID:90385285; PMID:2402639
 A:Accession: A35844
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: mRNA
 A:Residues: 1-2524 <COP>
 C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
 C:Keywords: transmembrane protein
 F:146-177/Domain: EGF homology <EGX1>
 F:184-215/Domain: EGF homology <EGF1>
 F:222-254/Domain: EGF homology <EGF1>
 F:436-487/Domain: EGF homology <EGX2>
 F:757-788/Domain: EGF homology <EGF3>
 F:1025-1056/Domain: EGF homology <EGX3>
 F:1924-1956/Domain: ankyrin repeat homology <AN1>
 F:1957-1989/Domain: ankyrin repeat homology <AN2>
 F:1991-2023/Domain: ankyrin repeat homology <AN3>
 F:2024-2056/Domain: ankyrin repeat homology <AN4>
 F:2057-2089/Domain: ankyrin repeat homology <AN5>

Query Match 40.0%; Score 56; DB 2; Length 2524;
 Best Local Similarity 40.9%; Pred. No. 14;
 Matches 9; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 6 QKCFQHLDDCCSXCNXXNCV 27
 Db 252 QNCEINIDCPSNCRNGCTCV 273

RESULT 4

A24420
 notch protein - fruit fly (Drosophila melanogaster)
 N:Alternate names: neurogenic repetitive locus protein
 C:Species: Drosophila melanogaster
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A24420; A24768; S09358; A05267
 R:Kidd, S.; Kelley, M.R.; Young, M.W.
 Mol. Cell. Biol. 6, 3094-3108, 1986
 A:Reference number: A24420; MUID:87064624; PMID:3097517
 A:Accession: A24420

A:Molecule type: DNA
 A:Residues: 1-2703 <KID>
 A:Cross-references: GB:K03508; NID:g157991; PIDN:AAA28725.1; PID:g157993
 R:Wharton, K.A.; Johansen, K.M.; Xu, T.; Arcavanis-Tsakonas, S.
 Cell 43, 567-581, 1985
 A:Reference number: A24768; MUID:86079539; PMID:3935325
 A:Accession: A24768
 A:Molecule type: mRNA

A:Residues: 1-48, 'I', 50-118, 'R', 120-230, 'I', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-9
 A:Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2
 R:Nautz, D.
 Nucleic Acids Res. 17, 6463-6471, 1989

A:Title: Hypervariability of simple sequences as a general source for polymorphic DNA
 A:Reference number: S09358; MUID:89385974; PMID:2780284
 A:Accession: S09358
 A:Molecule type: DNA
 A:Residues: 2505-2551, 'Q'Q'Q', 2552-2576, 'E', 2578-2604 <TAU>
 R:Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Arcavanis-Tsakonas, S.
 Cell 40, 55-62, 1985

A:Title: opa: a novel family of transcribed repeats shared by the Notch locus and oth
 A:Reference number: A05267; MUID:85093929; PMID:2981631
 A:Accession: A05267
 A:Molecule type: DNA
 A:Residues: 2504-2576, 'E', 2578-2611 <MHA2>

C:Genetics:
 A:Gene: notch; opa
 A:Cross-references: FlyBase:FBgn0004647
 A:Map position: 8.96-9.36

C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
 C:Keywords: differentiation; tandem repeat; transmembrane protein
 F:27-43/Domain: transmembrane #status predicted <TMN1>
 F:297-328/Domain: EGF homology <EGX1>
 F:530-561/Domain: EGF homology <EGF1>
 F:568-599/Domain: EGF homology <EGF>
 F:988-1019/Domain: EGF homology <EGX2>

F:1064-1095/Domain: EGF homology <EGF3>
 F:1187-1218/Domain: EGF homology <EGX3>
 F:1746-1762/Domain: transmembrane #status predicted <TMN2>
 F:1950-1982/Domain: ankyrin repeat homology <AN1>
 F:1983-2015/Domain: ankyrin repeat homology <AN2>
 F:1988-2004/Domain: transmembrane #status predicted <TMN3>

F:2017-2049/Domain: ankyrin repeat homology <AN3>
 F:2050-2082/Domain: ankyrin repeat homology <AN4>
 F:2083-2115/Domain: ankyrin repeat homology <AN5>
 F:2538-2568/Domain: glutamine-rich
 F:2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>

Query Match 39.3%; Score 55; DB 1; Length 2703;
 Best Local Similarity 36.4%; Pred. No. 19;
 Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 6 QKCFQHLDDCCSXCNXXNCV 27
 Db 824 QKCFINIDCVTPNCGNGCTCI 845

RESULT 5

T09059
 notch4 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jan-2000
 C:Accession: T09059
 R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.;
 submitted to the EMBL Data Library, October 1997

A:Description: Sequence of the mouse major histocompatibility locus class III region.
 A:Reference number: Z16543
 A:Accession: T09059
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-1964 <ROW>
 A:Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564947
 C:Genetics:

A:Gene: notch4
 A:Map position: 17
 A:Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1;
 1679/3; 1729/1; 1761/3
 C:Superfamily: unassigned EGF-related proteins; EGF homology
 C:Keywords: receptor; signal transduction
 F:514-545/Domain: EGF homology <EGF>

Query Match 37.1%; Score 52; DB 2; Length 1964;
Best Local Similarity 35.0%; Pred. No. 37;
Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 8 CF0HLDDCCSXXCNXXNKC 27
| : : | | | : | : | : |
DB 349 CEENIDDCAAATCAFGSTCI 368

RESULT 6

S42612
transmembrane protein precursor - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002
C:Accession: S42612
R:Bierkamp, C.; Campos-Ortega, J.A.
Mol. Dev. 43, 87-100, 1993
A:Title: A zebrafish homolog of the Drosophila neurogenic gene Notch and its pattern
A:Reference number: S42612; MUID:94128602; PMID:8297791
A:Accession: S42612
A:Molecule type: mRNA
A:Residues: 1-2437 <BIE>
A:Status: preliminary
A:Cross-references: EMBL:X69088; NID:9433866; PIDD:CAA48831.1; PID:9433867
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:755-786/Domain: EGF homology <EGF1>
F:1023-1054/Domain: EGF homology <EGF2>
F:1185-1216/Domain: EGF homology <EGF3>
F:1915-1947/Domain: ankyrin repeat homology <AN1>
F:1948-1980/Domain: ankyrin repeat homology <AN2>
F:1982-2014/Domain: ankyrin repeat homology <AN3>
F:2015-2047/Domain: ankyrin repeat homology <AN4>
F:2048-2080/Domain: ankyrin repeat homology <AN5>

Query Match 37.1%; Score 52; DB 2; Length 2437;
Best Local Similarity 36.8%; Pred. No. 43;

Matches 7; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 8 CF0HLDDCCSXXCNXXNKC 26
| : : | | | : | : | : |
DB 331 CSENIIDDCASACSHGATC 349

RESULT 7

A40043
notch protein homolog TAN-1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 02-Aug-2002
C:Accession: A40043
R:Ellisen, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, T.C.; Smith, S.D.; Sklar, Cell 66, 649-661, 1991
A:Title: TAN-1, the human homolog of the Drosophila Notch gene, is broken by chromosomal
A:Reference number: A40043; MUID:1347367; PMID:1831692
A:Accession: A40043
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-2555
A:Cross-references: GB:M73980
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:261-292/Domain: EGF homology <EGF1>
F:494-525/Domain: EGF homology <EGF2>
F:987-1018/Domain: EGF homology <EGF3>
F:1148-1180/Domain: EGF homology <EGF4>
F:1187-1218/Domain: EGF homology <EGF5>
F:1233-1264/Domain: EGF homology <EGF6>
F:1927-1959/Domain: ankyrin repeat homology <AN1>
F:1960-1992/Domain: ankyrin repeat homology <AN2>
F:1994-2026/Domain: ankyrin repeat homology <AN3>
F:2027-2059/Domain: ankyrin repeat homology <AN4>
F:2060-2092/Domain: ankyrin repeat homology <AN5>

Query Match 37.1%; Score 52; DB 2; Length 2555;
Best Local Similarity 36.4%; Pred. No. 45;

Matches 8; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

OY 6 QKCF0HLDDCCSXXCNXXNKC 27
| : : | | | : | : | : |
DB 252 QNCEENIDDCPGNNCKNGACV 273

RESULT 8

S18188
notch protein homolog - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C:Accession: S18188
R:Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development 113, 199-205, 1991
A:Title: A homolog of Drosophila Notch expressed during mammalian development.
A:Reference number: S18188; MUID:92111383; PMID:1764995
A:Accession: S18188
A:Molecule type: mRNA
A:Residues: 1-2531 <WEI>
A:Status: preliminary
A:Cross-references: EMBL:X57405; NID:957634; PID:957635
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:987-1018/Domain: EGF homology <EGF1>
F:1025-1056/Domain: EGF homology <EGF2>
F:1233-1264/Domain: EGF homology <EGF3>
F:1917-1949/Domain: ankyrin repeat homology <AN1>
F:1950-1982/Domain: ankyrin repeat homology <AN2>
F:1984-2016/Domain: ankyrin repeat homology <AN3>
F:2017-2049/Domain: ankyrin repeat homology <AN4>
F:2050-2082/Domain: ankyrin repeat homology <AN5>

Query Match 36.4%; Score 51; DB 2; Length 2531;
Best Local Similarity 36.4%; Pred. No. 59;

Matches 8; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

OY 6 QKCF0HLDDCCSXXCNXXNKC 27
| : : | | | : | : | : |
DB 252 QNCEENIDDCPGNNCKNGACV 273

RESULT 9

A46019
Notch-1 protein - mouse
N:Alternate names: notch protein
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Sep-1999
C:Accession: A46019; S25144
R:del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; G.
Genomics 15, 259-264, 1993
A:Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog
A:Reference number: A46019; MUID:93194170; PMID:8449489
A:Accession: A46019
A:Status: not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-2531
A:Cross-references: GB:Z11886; GB:S47228; NID:9288502; PIDD:CAA77941.1; PID:9288503
A:Note: sequence extracted from NCBI backbone (NCBIP:127318)
R:Francisco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.
submitted to the EMBL Data Library, April 1992
A:Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, sug
A:Reference number: S25144
A:Accession: S25144
A:Molecule type: mRNA
A:Residues: 1551-2108, 'Q', 2110-2114, 'ALP', 2118-2170 <FRA>
A:Cross-references: EMBL:Z11886
C:Genetics:
A:Gene: notch-1
A:Map position: 2
A:Note: proximal region of chromosome 2
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol
F:106-138/Domain: EGF homology <EGF1>
F:144-175/Domain: EGF homology <EGF2>
F:222-254/Domain: EGF homology <EGF3>

F:261-292/Domains: EGF homology <EG02>
 F:339-370/Domains: EGF homology <EG03>
 F:416-449/Domains: EGF homology <EGF3>
 F:456-487/Domains: EGF homology <EG04>
 F:494-525/Domains: EGF homology <EG05>
 F:532-563/Domains: EGF homology <EG06>
 F:607-638/Domains: EGF homology <EG07>
 F:682-713/Domains: EGF homology <EG08>
 F:757-788/Domains: EGF homology <EG09>
 F:795-826/Domains: EGF homology <EG10>
 F:873-904/Domains: EGF homology <EG11>
 F:911-942/Domains: EGF homology <EG12>
 F:949-980/Domains: EGF homology <EG13>
 F:987-1018/Domains: EGF homology <EG14>
 F:1025-1056/Domains: EGF homology <EG15>
 F:1063-1094/Domains: EGF homology <EG16>
 F:1148-1180/Domains: EGF homology <EG17>
 F:1187-1218/Domains: EGF homology <EG18>
 F:1233-1264/Domains: EGF homology <EG19>
 F:1352-1383/Domains: EGF homology <EG20>
 F:1391-1425/Domains: EGF homology <EG21>
 F:1917-1948/Domains: ankyrin repeat homology <AN1>
 F:1949-1981/Domains: ankyrin repeat homology <AN2>
 F:1983-2015/Domains: ankyrin repeat homology <AN3>
 F:2016-2048/Domains: ankyrin repeat homology <AN4>
 F:2049-2081/Domains: ankyrin repeat homology <AN5>

Query Match 36.4%; Score 51; DB 2; Length 2531;
 Best Local Similarity 36.4%; Pred. No. 59;

Matches 8; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 6 OKCFQHLDDCCSXKCNXKCV 27
 Db 252 ONCEENVDDCCPGNCKNGACV 273

RESULT 10

Omega-conotoxin MVIC precursor [validated] - cone shell (Conus magus) (fragment)

C/Species: Conus magus (magus cone)

C/Date: 17-Apr-1993 #sequence_revision 11-Apr-1997 #text_change 15-Sep-2000

C/Accession: JH0699; PC2380

R/Hillyard, D.R.; Monje, V.D.; Miltz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; M

Neuron 9, 69-77, 1992

A/Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.

A/Reference number: JH0699; MUID:92337922; PMID:1352986

A/Accession: JH0699

A/Molecule type: mRNA

A/Residues: 1-29 <HL>

A/Cross-references: GB:S40826; NID:9252126; PIDN:AB22674.1; PID:9252127

R/Nemoto, N.; Kubo, S.; Yoshida, T.; Chino, N.; Kimura, T.; Sakakibara, S.; Kyogoku, Y.;

Biochem. Biophys. Res. Commun. 207, 695-700, 1995

A/Title: Solution structure of omega-conotoxin MVIC determined by NMR.

A/Reference number: PC2380; MUID:95169113; PMID:7864862

A/Accession: PC2380

A/Molecule type: protein

A/Residues: 3-28 <ME>

R/Parr-Jones, S.; Basus, V.J.

submitted to the Brookhaven Protein Data Bank, December 1994

A/Reference number: A66297; PDB:1OMN

A/Contents: annotation: conformation by (1)H-NMR, residues 3-28

R/Parr-Jones, S.; Mijangich, G.P.; Nadasdi, L.; Ramachandran, J.; Basus, V.J.

J. Mol. Biol. 248, 106-124, 1995

A/Title: Solution structure of omega-conotoxin MVIC, a high affinity of P-type calcium

A/Reference number: A58582; MUID:95248539; PMID:7732037

A/Contents: annotation: conformation by (1)H-NMR

C/Superfamily: omega-conotoxin

C/Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh

F:3-28/Product: omega-conotoxin MVIC #status experimental <MAT>

F:3-18,10-22,17-28/Disulfide bonds: #status experimental

F:28/Modified site: amidated carboxyl end (Cys) (amide in mature form from following gly

Best Local Similarity 30.8%; Pred. No. 4.2;
 Matches 8; Conservative 3; Mismatches 15; Indels 0; Gaps 0;

Qy 1 CRINOKFOHLDDCCSXKCNXKCV 26
 Db 3 CKGNAPCRKTMVDDCCSGSGRGKC 28

RESULT 11

hypoetical protein F46B3.9 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C/Accession: T22274

R/Almsrough, R.

submitted to the EMBL Data Library, November 1996

A/Reference number: Z19541

A/Accession: T22274

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-354 <MT>

A/Cross-references: EMBL:281540; PIDN:CA804398.1; GSPDB:GN00023; CESP:F46B3.9

A/Experimental source: clone F46B3

C/Genetics:

A/Map position: 5

A/Insertions: 23/1; 55/1; 82/1; 112/1; 142/1; 170/1; 193/1; 223/1; 299/1

Query Match 35.7%; Score 50; DB 2; Length 354;
 Best Local Similarity 32.1%; Pred. No. 22;

Matches 9; Conservative 4; Mismatches 13; Indels 2; Gaps 1;

Qy 1 CRINX--OKCFQHLDDCCSXKCNXKCV 26
 Db 158 CKLVGSPKCPVLDQCSHKISGSHC 185

RESULT 12

A/9175

Notch B protein - mouse (fragment)

N/Alternate names: Notch homolog

C/Species: Mus musculus (house mouse)

C/Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 20-Sep-1999

C/Accession: A49175; P1570; S32113

R/Lardelli, M.; Lendahl, U.

Exp. Cell Res. 204, 364-372, 1993

A/Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety

A/Reference number: A49175; MUID:93178563; PMID:8440332

A/Accession: A49175

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-1203 <LAR>

A/Cross-references: EMBL:X68279; NID:9287989; PIDN:CAA48340.1; PID:9287990

A/Experimental source: embryo

A/Note: sequence extracted from NCBI backbone (NCBI:P126158)

C/Comment: This protein has many EGF repeats and 11n-12/Notch repeats.

C/Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol

F:143-174/Domains: EGF homology <EGX1>

F:482-513/Domains: EGF homology <EGF1>

F:560-591/Domains: EGF homology <EGF2>

F:674-705/Domains: EGF homology <EGX2>

F:712-743/Domains: EGF homology <EGF3>

F:836-867/Domains: EGF homology <EGX3>

Query Match 35.7%; Score 50; DB 2; Length 1203;
 Best Local Similarity 30.0%; Pred. No. 49;
 Matches 6; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 8 CFQHLDDCCSXKCNXKCV 27
 Db 18 CSENIDCAVASCPSGSL 37

RESULT 13

A49128

cell-fate determining gene Notch2 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002

C:Accession: A49128

R:Wilmaster, G.; Roberts, V.J.; Lemke, G.

Development 116, 931-941, 1992

A:Title: Notch2: a second mammalian Notch gene.

A:Reference number: A49128; MUID:93202015; PMID:1295745

A:Accession: A49128

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-2471 <MEI>

A:Experimental source: Schwann cell

C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

F:264-295/Domain: EGF homology <EGX1>

F:799-830/Domain: EGF homology <EGF1>

F:877-908/Domain: EGF homology <EGX2>

F:1029-1060/Domain: EGF homology <EGF>

F:1067-1098/Domain: EGF homology <EGX3>

F:1153-1184/Domain: EGF homology <EGF3>

F:1191-1222/Domain: EGF homology <EGX4>

F:1876-1908/Domain: ankyrin repeat homology <AN1>

F:1909-1941/Domain: ankyrin repeat homology <AN2>

F:1943-1975/Domain: ankyrin repeat homology <AN3>

F:1976-2008/Domain: ankyrin repeat homology <AN4>

F:2009-2041/Domain: ankyrin repeat homology <AN5>

Query Match

Best local Similarity

Matches

6; Conservative

5; Mismatches

9; Indels

0; Gaps

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RESULT 14

E86452

protein F6N18.15 [Imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: E86452

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

Nansen, N.F.; Hughes, B.; Hultzar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, J.C.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: E86452

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STO>

A:Cross-references: GB:AE005172; NID:g6714280; PIDN:AAF25976.1; GSPDB:GN00141

C:Genetics:

A:Gene: F6N18.15

A:Map position: 1

Query Match

Best local Similarity

Matches

7; Conservative

4; Mismatches

4; Indels

0; Gaps

0;

RESULT 15

T22025

hypochemical protein F40E10.4 - Caenorhabditis elegans (fragment)

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T22025

R:Smey, R.

submitted to the EMBL Data Library, February 1996

A:Reference number: Z19503

A:Accession: T22025

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-601 <WIL>

A:Cross-references: EMBL:Z69792; PIDN:CAA93668.1; GSPDB:GN00028; CESP:F40E10.4

A:Experimental source: clone F40E10

C:Genetics:

A:Gene: CESP:F40E10.4

A:Map position: X

Query Match

Best local Similarity

Matches

7; Conservative

4; Mismatches

9; Indels

0; Gaps

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Search completed: January 14, 2003, 18:29:27
Job time : 17 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 18:17:10 ; Search time 11 Seconds

(without alignments)
101.806 Million cell updates/sec

Title: US-09-666-837B-1-COPY

Perfect score: 140
Sequence: 1 CRXNQCfQhLDCCSXXCNXNXC 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	127	90.7	72	1	CKX7_CONPU
2	60	42.9	72	1	CKOB_CONST
3	56	40.0	2524	1	NORC_XENLA
4	55	39.3	26	1	CKOC_CONCT
5	55	39.3	2703	1	NORC_DROME
6	53	37.9	73	1	CKOD_CONCT
7	52	37.1	1964	1	NTC4_MOUSE
8	52	37.1	2437	1	NTC1_BRARE
9	52	37.1	2556	1	NTC1_HUMAN
10	51	36.4	589	1	DL3_RAT
11	51	36.4	592	1	DL3_MOUSE
12	51	36.4	618	1	DL3_HUMAN
13	51	36.4	2003	1	NTC4_HUMAN
14	51	36.4	2531	1	NTC1_MOUSE
15	51	36.4	2531	1	NTC1_RAT
16	50	35.7	29	1	CKOC_CONMA
17	50	35.7	2470	1	NTC2_MOUSE
18	50	35.7	2471	1	NTC2_HUMAN
19	50	35.7	2471	1	NTC2_RAT
20	49	35.0	1202	1	JAG2_RAT
21	49	35.0	1238	1	JAG2_HUMAN
22	49	35.0	1247	1	JAG2_MOUSE
23	49	35.0	2318	1	NTC3_MOUSE
24	49	35.0	2319	1	NTC3_RAT
25	49	35.0	2321	1	NTC3_HUMAN
26	48	34.3	2139	1	CRB_DROME
27	47.5	33.9	53	1	CTLI_NPVOP
28	47	33.6	71	1	CKOA_CONMA
29	47	33.6	723	1	DL1_HUMAN
30	47	33.6	833	1	DL_DROME
31	47	33.6	1064	1	FBPI_STRPU
32	47	33.6	1480	1	SLIT_DROME
33	46.5	33.2	53	1	CTLI_NPVAC

34	46	32.9	25	1	CKOB_CONMA	P05485	conus magus
35	46	32.9	644	1	YGM4_YEAST	P53129	saccharomyc
36	46	32.9	714	1	DL1_RAT	P97677	rattus norv
37	46	32.9	722	1	DL1_MOUSE	O61483	mus musculu
38	45	32.1	29	1	CKOD_CONMA	O26350	conus magus
39	45	32.1	399	1	LHX5_BRARE	P52889	brachydantio
40	45	32.1	570	1	FBP3_STRPU	P49013	strongyloce
41	45	32.1	1213	1	JAG3_BRARE	O90954	brachydantio
42	45	32.1	1218	1	JAG1_HUMAN	P78504	homo sapien
43	45	32.1	1218	1	JAG1_MOUSE	O9qxx0	mus musculu
44	44	31.4	268	1	IL1B_RABIT	P14628	oryctolagus
45	44	31.4	402	1	LHX5_XENLA	P37137	xenopus lae

ALIGNMENTS

RESULT 1
CKX7_CONPU STANDARD; PRT; 72 AA.
AC P56633;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Kappa-conotoxin PVIIA precursor (Pin-popping peptide).
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
NCBI_TaxID=41690;
RN [1]
RP SEQUENCE FROM N.A., AND SYNTHESIS.
RX MEDLINE=98079023; PubMed=9417043;
RA Shon K.-J., Stocker M., Terlau H., Stuehmer W., Jacobsen R.B.,
Walker C.S., Grille M.M., Watkins M., Hillyard D.R., Gray W.R.,
Olivera B.M.;
RT "Kappa-conotoxin PVIIA is a peptide inhibiting the shaker K+
channel.";
RL J. Biol. Chem. 273:33-38(1998).
RN [2]
RP SEQUENCE OF 46-72, AND SYNTHESIS.
RX PubMed=12074021;
RA Terlau H., Shon K.-J., Grille M.M., Stocker M., Stuehmer W.,
Olivera B.M.;
RT "Strategy for rapid immobilization of prey by a fish-hunting marine
snail.";
RL Nature 381:148-151(1996).
RN [3]
RP STRUCTURE BY NMR.
RX TISSUE=Venom;
MEDLINE=98104087; PubMed=9438859;
RA Scanlon M.J., Naranjo D., Thomas L., Alewood P.F., Lewis R.J.,
Craik D.J.;
RT "Solution structure and proposed binding mechanism of a novel
potassium channel toxin kappa-conotoxin PVIIA.";
RL Structure 5:1585-1597(1997).
RN [4]
RP STRUCTURE BY NMR.
MEDLINE=98217295; PubMed=9548922;
RX Savarin P., Guenouves M., Gilquin B., Lamthanh H., Gasparini S.,
Zinn-Justin S., Menez A.;
RT "Three-dimensional structure of kappa-conotoxin PVIIA, a novel
potassium channel-blocking toxin from cone snails.";
RL Biochemistry 37:5407-5416(1998).
RN [5]
RP MUTAGENESIS OF ARG-47; ILE-48; PRO-49; ASN-50; GLN-51; PHE-54;
PHE-54; GLN-55; HIS-56; LEU-57; ASP-58; ASP-59; SER-62; ARG-63;
LYS-64; ARG-67; PHE-68; ASN-69 AND LYS-70.
RX PubMed=10818067;
RA Jacobsen R.B., Koch E.D., Lange-Malecki B., Stocker M., Verhey J.,
Van Wagoner R.M., Vozovkina A., Olivera B.M., Terlau H.;
RT "Single amino acid substitutions in kappa-conotoxin PVIIA disrupt
interaction with the shaker K+ channel.";
RL J. Biol. Chem. 275:24639-24644(2000).

RP	[6]	BLOCKADE OF SHAKER CHANNEL BY PVIIA.
RX	PubMed-10398696.	
RA	Tertlau H., Boccaccio A., Olivera B.M., Conti F.;	
RT	"The block of Shaker K ⁺ channels by kappa-conotoxin PVIIA is state dependent.";	
RL	J. Gen. Physiol. 114:125-140(1999).	
RN	[7]	
RP	MODEL OF THE SHAKER-PVIIA INTERACTION.	
RX	PubMed-11820396;	
RA	Moran O.;	
RT	"Molecular simulation of the interaction of kappa-conotoxin-PVIIA with the Shaker potassium channel pore.";	
RL	Eur. Biophys. J. 30:528-536(2001).	
RN	[8]	
RP	BLOCKADE OF SHAKER CHANNEL BY PVIIA.	
RX	PubMed-12023223;	
RA	Narano D.;	
RT	"Inhibition of single Shaker K channels by kappa-conotoxin-PVIIA.";	
RL	Biophys. J. 82:3003-3011(2002).	
CC	-1- FUNCTION: kappa-conotoxins bind and inhibit voltage-sensitive potassium channels. The rat brain voltage-gated potassium channel protein Kv1.1 is resistant to this toxin, but the voltage-gated potassium channel protein Shaker (Drosophila) is sensitive. The interaction site between the Shaker channel and this toxin is within the S5-S6 loop of the Shaker channel. In fish, this toxin induces hyperactivity, followed by continuous contraction and extension of major fins, without immobilization or death. Injection of this peptide together with the delta-conotoxin PVIA causes the sudden tetanus of prey (STOP) syndrome, which is a single, lethal "fin-pop" in envenomated fish. In mice, induces hyperactivity.	
CC	-1- SUBCELLULAR LOCATION: Secreted.	
CC	-1- TISSUE SPECIFICITY: Expressed by the venom duct.	
CC	-1- MASS SPECTROMETRY: MW=3268.4, METHOD=FAH.	
CC	-1- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS.	
CC	-1- CAUTION: Because analogs resulting of mutagenesis of Hyp-49, Asn-50, Leu-57 and Asp-59 gave very low yields upon folding, the results of mutagenesis on these residues should be interpreted with caution.	
DR	PDB: 1AV3: 18-NOV-98.	
KM	Neurotoxin; Toxin; Potassium channel inhibitor; Hydroxylation; 3D-structure; Signal.	
KW	SIGNAL	
FT	PROPER	1 22
FT	PEPTIDE	23 45
FT	DISULFID	46 72
FT	DISULFID	46 61
FT	DISULFID	53 65
FT	DISULFID	60 71
FT	MOD_RES	49 49
FT	MUTAGEN	47 47
FT	MUTAGEN	48 48
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FT	MUTAGEN	69 69
FT	MUTAGEN	70 70
FT	MUTAGEN	70 70
SEQUENCE	72 AA: 8317 MW: 538F979EE751C6 CRC64:	

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Query Match Summary          90.7%: Score 127; DB 1; Length 72;
Best Local Similarity       77.8%: Pred. No. 3e-11;
Matches    21; Conservative 0; Mismatches 6; Indels 0; Gaps 0

Qy      1 CRIXNCKCFQHLDDCCSXKXNKNXKCV 27
Db      46 CRIPNCKCFQHLDDCCSRKCNRFNKC 72

RESULT 2
CXOB_CONST
ID      CXOB_CONST      STANDARD:      PRT:      72 AA.
AC      P28881; Q9UB25;
DT      01-DEC-1992 (Rel. 24, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Omega-conotoxin SV1B precursor (SNX-183).
OS      Conus striatus (Striated cone).
OC      Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC      Neogastropoda; Conidae; Conus.
.OX      NCBI_TaxID=6493;
.RN      [1]
.RP      SEQUENCE FROM N.A.
.RC      TISSUE=Venom duct;
.RA      MEDLINE=20037955; PubMed=10573284;
.RA      Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
.RT      "Conopeptides from Conus striatus and Conus textile by cDNA
.RT      cloning.";
.RL      Peptides 20:1139-1144(1999).
.RN      [2]
.RP      SEQUENCE OF 46-71, AND SYNTHESIS.
.RC      TISSUE=Venom;
.RA      MEDLINE=93003172; PubMed=1390774;
.RA      Ramilo C., Zafarella G.C., Nadasdi L., Hammerland L.G., Yoshikami D.,
.RA      Gray W.R., Kristipati R., Ramachandran J., Miljanich G., Olivera B.M.,
.RA      Cruz L.J.;
.RT      "Novel alpha- and omega-conotoxins from Conus striatus venom.";
.RL      Biochemistry 31:9919-9926(1992).
.RN      [3]
.RP      STRUCTURE BY NMR.
.RA      MEDLINE=97070382; PubMed=8913308;
.RA      Nielsen K.J., Thomas L., Lewis R.J., Alewood P.F., Craik D.J.;
.RT      "A consensus structure for omega-conotoxins with different
.RT      selectivities for voltage-sensitive calcium channel subtypes:
.RT      comparison of MVIIA, SV1B and SNX-202.";
.RL      J. Mol. Biol. 263:297-310(1996).
.RN      -1- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
.RN      and block voltage-sensitive calcium channels (VSCC). This toxin
.RN      blocks N-, P-, and Q-type calcium channels.
.RN      -1- SUBCELLULAR LOCATION: Secreted.
.RN      -1- TISSUE SPECIFICITY: Expressed by the venom duct.
.RN      -1- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
.RN      FAMILY.
-----
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CC      or send an email to license@isb-sib.ch).
-----
CC      EMBL: AF146346; AAD31906.1; -
CC      PIR: C44379; C44379.
DR      PDB: 1MVU; 12-AUG-97.
DR      InterPro: IPR004214; Conotoxin.
DR      Pfam: PF02950; Conotoxin; 1.
KW      Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
KW      Amidation; Signal; 3D-structure
FT      SIGNAL 1 22 POTENTIAL.
FT      PROPEP 23 45
FT      PEPTIDE 46 71 OMEGA-CONOTOXIN SV1B.
FT      DISULFID 46 61

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FT DISULFID 53 65
 FT DISULFID 60 71
 FT MOD.RES 71 71
 SO SEQUENCE 72 AA; 7741 MW; 1F753546AAD39908 CRC64;
 Query Match 42.9%; Score 60; DB 1; Length 72;
 Best Local Similarity 34.6%; Pred. No. 0.044;
 Matches 9; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
 Oy 1 CRXNOKFOHLDCCSGSXCNXXNC 26
 Db 46 CKLKGSCRTSTDCSGSGCRGK 71
 RESULT 3
 NOTC_XENLA STANDARD; PRT: 2524 AA.
 AC P21783;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neurogenic locus notch protein precursor (XOTCH protein).
 GN XOTCH.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90385285; PubMed=2402639;
 RA Coffman C., Harris W., Kintner C.;
 RT "Xotch, the xenopus homolog of Drosophila notch."; Science 249:1438-1441(1990).
 RL Science 249:1438-1441(1990).
 RN [2]
 RP REVISIONS TO 1759-1782.
 RA Kintner C.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED ALMOST UNIFORMLY IN EARLY EMBRYOS.
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
 CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
 CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
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 CC -----
 DR EMBL: M33874; AAB02039.1; -
 DR PIR: A35844; A35844.
 DR HSP: P00740; IEDM.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF-2.
 DR InterPro: IPR001881; EGF_CA.
 DR InterPro: IPR001438; EGF-IT.
 DR InterPro: IPR000800; Notch.
 DR Pfam: PF00008; EGF; 36.
 DR Pfam: PF00023; ank; 6.
 DR Pfam: PF00066; notch; 3.
 DR PRINTS: PR00010; EGFBL00.
 DR PRINTS: PR01452; NOTCH.
 DR SMART: SM00248; ANK; 5.
 DR SMART: SM00179; EGF_CA; 23.
 DR SMART: SM00001; EGF-like; 11.
 DR SMART: SM00004; NL; 2.
 DR PROSITE: PS50088; ANK_REPEAT; 4.

DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
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 DR PROSITE: PS00022; EGF_1; 34.
 DR PROSITE: PS01186; EGF_2; 29.
 DR PROSITE: PS01187; EGF_CA; 21.
 KW Differentiation; Neurogenesis; Repeat; ANK repeat; EGF-like domain; Transmembrane; Signal; Glycoprotein.
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Query Match 40.0%; Score 56; DB 1; Length 2524;
 Best Local Similarity 40.9%; Pred. No. 2.8;

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Matches 9; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
OY 6 OKCFQHLDDCCSXKXNXXNCV 27
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Db 251 ONCEENIDCPNSNCRNGTCV 272

RESULT 4
CXOC_CONCT STANDARD; PRT; 26 AA.
AC PS8919;
DT 15-JUN-2002 (Rel. 41, Created)
DE 15-JUN-2002 (Rel. 41, Last sequence update)
DE Omega-conotoxin CVIC.
OS Conus catus (Cat cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Venom;
RX PubMed=10938268;
RA Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A.,
RA Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,
RA Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.;
RT "Novel omega-conotoxins from Conus catus discriminate among neuronal
RT calcium channel subtypes."
RL J. Biol. Chem. 275:33335-33344(2000).
CC -I- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
CC and block voltage-sensitive calcium channels (VSCC) (By
CC similarity). This toxin blocks N-, P-, and Q-type calcium
CC channels.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -I- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
CC FAMILY.
KW Presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
KW Amidation.
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FT DISULFID 26 26 AMIDATION.
SQ MOD_RES 26 AA; 2790 MW; 56EFC382335C4A8B CRC64;
SQ SEQUENCE 26 AA; 2790 MW; 56EFC382335C4A8B CRC64;

Query Match 39.3%; Score 55; DB 1; Length 26;
Best Local Similarity 30.8%; Pred. No. 0.094; Mismatches 13; Indels 0; Gaps 0;
Matches 8; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
OY 1 CRXNOKCFQHLDDCCSXKXNXXNC 26
| | : : : | | | | |
Db 1 CKKGQSCSKMYDCCTGSCSRGKC 26

RESULT 5
NOTC_DROME STANDARD; PRT; 2703 AA.
ID NOTC_DROME AC P07207; P04154; O97458; O9W4T8;
DT 01-NOV-1986 (Rel. 03, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurogenic locus Notch protein precursor.
GN N OR EG:140611.1 OR EG:163A10.2 OR CG3936.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Preygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Oregon-R; TISSUE=Embryo;
RX MEDLINE=86079539; PubMed=3935325;
RA Wharton K.A., Johansen K.M., Xu T., Artavanis-Tsakonas S.;

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RT "Nucleotide sequence from the neurogenic locus notch implies a gene
RT product that shares homology with proteins containing EGF-like
RT repeats."
RL Cell 43:567-581(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Canton-S, and Oregon-R: TISSUE-Embryo;
RX MEDLINE=87064624; PubMed=3097517;
RA Kidd S., Kelley M.R., Young M.W.;
RT "Sequence of the notch locus of Drosophila melanogaster: relationship
RT of the encoded protein to mammalian clotting and growth factors."
RL Mol. Cell. Biol. 6:3094-3108(1986).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-Oregon R;
RX MEDLINE=20196011; PubMed=10731137;
RA Benos P.V., Galt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrill B.G., Ferraz C., Vidal S., Brun C., Demallies F., Cadieu E.,
RA Dreano S., Gloux S., lelaure V., Mottier S., Galibert F., Borzova D.,
RA Minana B., Kafatos F.C., Louis C., Siden-Klamos I., Bolshakov S.,
RA Papagiannakis G., Spanos L., Cox S., Madeno E., de Pablos B.,
RA Modellell J., Peter A., Schoettler P., Warner M., Mourllocl F.,
RA Belnert N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of D.
RT melanogaster."
RL Science 287:2220-2222(2000).
RN [5]
RP SEQUENCE OF 2505-2611 FROM N.A.
RX MEDLINE=85099329; PubMed=2981631;
RA Wharton K.A., Yevonich B., Finerty V.G., Artavanis-Tsakonas S.;
RT "opa: a novel family of transcribed repeats shared by the Notch locus
RT and other developmentally regulated loci in D. melanogaster."
RL Cell 40:55-62(1985).
RN [6]
RP SEQUENCE OF 1-8 FROM N.A.
RX MEDLINE=87257846; PubMed=3037327;
RA Kelley M.R., Kidd S., Berg R.L., Young M.W.;
RT "Restriction of P-element insertions at the Notch locus of Drosophila
RT melanogaster."
RL Mol. Cell. Biol. 7:1545-1548(1987).
RN [7]
RP REVIEW.
RA Harris W.A.;
RT "Many cell types specified by Notch function."
RL Curr. Biol. 1:120-122(1991).
CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands Delta
CC and Serrate to regulate cell fate determination. Upon ligand
CC activation through the released notch intracellular domain (NICD)
CC it forms a transcriptional activator complex with Su(H)
CC (Suppressor of hairless) and activates genes of the enhancer of
CC split locus. Essential for proper differentiation of ectoderm.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
CC -----
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CC -----
DR EMBL: M16152; AAB59220.1; JOINED.
DR EMBL: M16153; AAB59220.1; JOINED.
DR EMBL: M16149; AAB59220.1; JOINED.
DR EMBL: M16150; AAB59220.1; JOINED.
DR EMBL: M16151; AAB59220.1; JOINED.
DR EMBL: K03508; AAA28725.1; JOINED.
DR EMBL: M13689; AAA28725.1; JOINED.
DR EMBL: K03507; AAA28725.1; JOINED.
DR EMBL: AE003426; AAF45848.2; JOINED.
DR EMBL: AL035436; CAB37610.1; JOINED.
DR EMBL: M12175; AAA74496.1; JOINED.
DR EMBL: M16025; AAA28726.1; JOINED.
DR PIR: A24420; A24420.
DR PIR: A24768; A24768.
DR PIR: A05267; A05267.
DR HSSP: P00740; 1EDM.
DR PDBase: FB90004647; N.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000152; Asx_hydroxy1.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR000800; Notch.
DR Pfam: PF00008; EGF; 36.
DR Pfam: PF00023; ank; 6.
DR Pfam: PF00065; notch; 3.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR00011; EGF_LAMININ.
DR PRINTS: PR01452; NOTCH.
DR SMART: SM00248; ANK; 7.
DR SMART: SM00181; EGF_Ca; 36.
DR SMART: SM00179; EGF_Ca; 35.
DR SMART: SM00004; NL; 2.

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DR PROSITE; PS50088; ANK_REPEAT; 5.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 22.
 DR PROSITE; PS00022; EGF_1; 34.
 DR PROSITE; PS01186; EGF_2; 28.
 DR PROSITE; PS01187; EGF_CA; 21.
 KW Receptor; Transcription regulation; Activator; Differentiation;
 KW Developmental protein; Neurogenesis; Repeat; ANK repeat;
 KW EGF-like domain; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 44
 FT CHAIN 45 2703
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 FT DOMAIN 1767 2703
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 FT DOMAIN 217 253
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 FT DOMAIN 293 329
 FT DOMAIN 331 370
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 FT DOMAIN 449 486
 FT DOMAIN 488 524
 FT DOMAIN 526 562
 FT DOMAIN 564 600
 FT DOMAIN 602 637
 FT DOMAIN 639 675
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 FT DOMAIN 867 905
 FT DOMAIN 907 944
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 Best Local Similarity 36.4%; Pred. No. 4;
 Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 6 QKCFHLDCCSXKXKXKCV 27
 DB 824 QKCFHLDCCSXKXKXKCV 845
 RESULT 6
 CXOD_CONCT STANDARD; PRT; 73 AA.
 AC P58920;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Omega-conotoxin CVID precursor.
 OS Conus catus (Cat cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 ON NCBI_Taxid=101291;
 RP SEQUENCE FROM N.A., SEQUENCE OF 46-72, SYNTHESIS, AND STRUCTURE BY
 RP NMR.
 RC TISSUE=Venom duct, and Venom;
 RX PubMed=10938268;
 RA Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A.,
 RA Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,
 RA Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.;
 RT "Novel omega-conotoxins from Conus catus discriminate among neuronal
 RT calcium channel subtypes";
 RL J. Biol. Chem. 275:35335-35344(2000).
 CC -1- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 CC and block voltage-sensitive calcium channels (VSCC) (by
 CC similarity). This toxin blocks N-type calcium channels.

CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
 CC FAMILY.
 KW presynaptic neurotoxin; Neurotoxin; Toxin; Calcium channel inhibitor;
 KW Amidation; Signal.
 FT SIGNAL 1 22
 FT PROPEP 23 45
 FT PEPTIDE 46 72
 FT DISULFID 46 61
 FT DISULFID 53 65
 FT DISULFID 60 72
 FT MOD_RES 72 72
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OY 1 CRXNORCFHLDCCSXKN 21
 DB 46 CRXNORCFHLDCCSXKN 66
 RESULT 7
 NTCA_MOUSE STANDARD; PRT; 1964 AA.
 AC P31695; O62389; O62390; O35442; Q9RLW9; O88314; O88316; Q9RLX0;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neurogenic locus notch homolog protein 4 precursor (Notch 4)
 DE [Contains: Transforming protein Int-3].
 GN NOTCH4 OR INT3 OR INT-3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92194507; PubMed=1312643;
 RA Robbins J., Blondel B.J., Gallahan D., Gallahan R.;
 RT "Mouse mammary tumor gene int-3: a member of the notch gene family
 RT transforms mammary epithelial cells.";
 RL J. Virol. 66:2594-2599(1992).
 RN [2]
 RP REVISIONS, SEQUENCE FROM N.A.
 RX MEDLINE=97294599; PubMed=9150355;
 RA Gallahan D., Gallahan R.;
 RT "The mouse mammary tumor associated gene INT3 is a unique member of
 RT the NOTCH gene family (NOTCH4).";
 RL Oncogene 14:1883-1890(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung, and Testis;
 RX MEDLINE=96281668; PubMed=8681805;
 RA Uytendaele H., Marazzi G., Wu G., Yan Q., Sassoon D., Kitajewski J.;
 RT "Notch4/int-3, a mammary proto-oncogene, is an endothelial
 RT cell-specific mammalian Notch gene.";
 RL Development 122:2251-2259(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Rowen L., Mahatras G., Qin S., Ahearn M.E., Dankers C., Lasky S.,
 RA Loretz C., Schmidt S., Tipton S., Tralcoff R., Zackrone K., Hood L.;
 RT "Sequence of the mouse major histocompatibility locus class III
 RT region.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1436-1600 FROM N.A.
 RX MEDLINE=99252212; PubMed=102333982;
 RA Lee J.-S., Haruna T., Ishimoto A., Honjo T., Yanagawa S.-I.;
 RT "Intracisternal type A particle-mediated activation of the Notch4/Int3
 RT gene in a mouse mammary tumor: generation of truncated Notch4/Int3

FT REPEAT 1168 1208 LIN/NOTCH 1.
 FT REPEAT 1209 1242 LIN/NOTCH 2.
 FT REPEAT 1243 1282 LIN/NOTCH 3.
 FT REPEAT 1628 1657 ANK 1.
 FT REPEAT 1661 1691 ANK 2.
 FT REPEAT 1695 1724 ANK 3.
 FT REPEAT 1728 1757 ANK 4.

 Query Match 37.18; Score 52; DB 1; Length 1964;
 Best Local Similarity 35.08; Pred. No. 7.9;
 Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

 QY 8 CF0HLDCCSXXCNXNKCXV 27
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 Db 349 CENMLDCCAAATCAFGSTCI 368

 RESULT 8
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 AC P46530;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neurogenic locus notch homolog protein 1 precursor.
 GN NOTCH1 OR NOTCH.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 RN NCBI_TaxID=7955;
 RX 1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=94128602; PubMed=8297791;
 RA Bierkamp C., Campos-Ortega J.A.;
 RT "A zebrafish homologue of the Drosophila neurogenic gene Notch and
 RL its pattern of transcription during early embryogenesis."; Mech. Dev. 43:87-100(1993).
 CC -1- FUNCTION: IMPLICATED IN CELL FATE SPECIFICATIONS DURING
 CC EMBRYO DEVELOPMENT. MAY BE INVOLVED IN THE FORMATION OF THE
 CC NEURAL PLATE, NOTOCHORD AND BRAIN VESTICLES.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DEVELOPMENTAL STAGE: Expressed in all cells in pregastrulation
 CC stages. During gastrulation is differentially expressed,
 CC accumulating predominantly in the prechordal mesoderm and
 CC notochord. At the end of gastrulation, expressed along the
 CC anterior-posterior axis including the developing neural plate
 CC and differentiating mesoderm. Also present in the developing
 CC brain and head regions.
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
 CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
 CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
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 CC -----
 DR EMBL: X65088; CAA4831.1; -;
 DR HSP: P00740; 1EDM;
 DR ZFIN: ZDR-GENE-990415-173; notch1a.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF_1like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_TI.
 DR InterPro: IPR000800; Notch.

DR Pfam: PF00008; EGF; 36.
 DR Pfam: PF00023; ank; 6.
 DR Pfam: PF00066; notch; 3.
 DR PRINTS: PR00010; EGFLOD.
 DR PRINTS: PR01452; NOTCH.
 DR SMART: SM00248; ANK; 5.
 DR SMART: SM00179; EGF_Ca; 19.
 DR SMART: SM00001; EGF_1like; 16.
 DR SMART: SM00004; NL; 3.
 DR PROSITE: PS50088; ANK_REPEAT; 4.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 23.
 DR PROSITE: PS00022; EGF_1; 34.
 DR PROSITE: PS01186; EGF_2; 28.
 DR PROSITE: PS01187; EGF_Ca; 22.
 KW Receptor; Transcription regulation; Activator; Differentiation;
 KW Developmental protein; Neurogenesis; Repeat; ANK repeat;
 KW EGF-like domain; Transmembrane; Glycoprotein; Signal.
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CLEAVAGE BY FUZIN-LIKE PROTEASE (BY
 SIMILARITY).
 BY SIMILARITY.

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FT DISULFID 47 56 BY SIMILARITY.
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FT DISULFID 439 448 BY SIMILARITY.
FT DISULFID 455 466 BY SIMILARITY.
FT DISULFID 460 475 BY SIMILARITY.
FT DISULFID 477 486 BY SIMILARITY.
FT DISULFID 493 503 BY SIMILARITY.
FT DISULFID 498 512 BY SIMILARITY.
FT DISULFID 514 523 BY SIMILARITY.
FT DISULFID 541 550 BY SIMILARITY.
FT DISULFID 530 550 BY SIMILARITY.
FT DISULFID 552 561 BY SIMILARITY.
FT DISULFID 568 578 BY SIMILARITY.
FT DISULFID 573 587 BY SIMILARITY.
FT DISULFID 589 598 BY SIMILARITY.
FT DISULFID 605 616 BY SIMILARITY.
FT DISULFID 610 625 BY SIMILARITY.
FT DISULFID 627 636 BY SIMILARITY.
FT DISULFID 643 653 BY SIMILARITY.
FT DISULFID 648 662 BY SIMILARITY.
FT DISULFID 664 673 BY SIMILARITY.
FT DISULFID 680 691 BY SIMILARITY.
FT DISULFID 685 700 BY SIMILARITY.
FT DISULFID 702 711 BY SIMILARITY.
FT DISULFID 718 728 BY SIMILARITY.
FT DISULFID 723 737 BY SIMILARITY.
FT DISULFID 739 748 BY SIMILARITY.
FT DISULFID 755 766 BY SIMILARITY.
FT DISULFID 760 775 BY SIMILARITY.
FT DISULFID 777 786 BY SIMILARITY.
FT DISULFID 793 804 BY SIMILARITY.
FT DISULFID 798 813 BY SIMILARITY.
FT DISULFID 815 824 BY SIMILARITY.
FT DISULFID 831 842 BY SIMILARITY.
FT DISULFID 836 853 BY SIMILARITY.
FT DISULFID 855 864 BY SIMILARITY.
FT DISULFID 871 882 BY SIMILARITY.
FT DISULFID 876 891 BY SIMILARITY.
FT DISULFID 893 902 BY SIMILARITY.
FT DISULFID 909 920 BY SIMILARITY.
FT DISULFID 914 929 BY SIMILARITY.
FT DISULFID 931 940 BY SIMILARITY.
FT DISULFID 947 958 BY SIMILARITY.
FT DISULFID 952 967 BY SIMILARITY.
FT DISULFID 969 978 BY SIMILARITY.

```

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Query Match 37.1%; Score 52; DB 1; Length 2437;
Best Local Similarity 36.8%; Pred. No. 9.5;
Matches 7; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 8 CF0HDDCCSXCNXXNC 26
Db 331 CSENIIDCASHGATC 349

RESULT 9
NTCL_HUMAN STANDARD; PRT; 2556 AA.
ID NTCL_HUMAN
AC P46531;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurogenic locus notch homolog protein 1 precursor (Notch 1) (hnl)
DE (Translocation-associated notch protein TAN-1).
GN NOTCH1 OR TAN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mann R.S., Blummueller C.M., Zagouras P.;
RT "Complete human notch 1 (hnl) cDNA sequence."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-2444 FROM N.A.
RA MEDLINE=91347367; PubMed=1831692;
RA Ellisen L.W., Bird D.C., Soreng A.L., Reynolds T.C.,
RA Smith S.D., Sclar J.;
RT "TAN-1, the human homolog of the Drosophila notch gene, is broken by
RT chromosomal translocations in T lymphoblastic neoplasms."
RL Cell 66:645-661(1991).
RN [3]
RP IDENTIFICATION OF LIGANDS.
RX MEDLINE=99180765; PubMed=10079256;
RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
RT Am. J. Pathol. 154:785-794(1999).
RL
CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands
CC Jagged1, Jagged2 and Delta1 to regulate cell-fate determination.
CC Upon ligand activation through the released notch intracellular
CC domain (NTCD) it forms a transcriptional activator complex with
CC RBP-J kappa and activates genes of the enhancer of split locus.
CC Affects the implementation of differentiation, proliferation and
CC apoptotic programs. May be important for normal lymphocyte
CC function. In altered form, may contribute to transformation or
CC progression in some T-cell neoplasms. Involved in the maturation
CC of both CD4+ and CD8+ cells in the thymus (By similarity).
CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TW) and a N-
CC terminal fragment N(EC) which are probably linked by disulfide
CC bonds (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following
CC proteolytical processing NICD is translocated to the nucleus (By
CC similarity).
CC -1- TISSUE SPECIFICITY: In fetal tissues most abundant in spleen,
CC brain stem and lung. Also present in most adult tissues where it
CC is found mainly in lymphoid tissues.
CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form
CC which is proteolytically cleaved by a furin-like convertase in the
CC trans-golgi network before it reaches the plasma membrane to yield
CC an active, ligand-accessible form. Cleavage results in a C-
CC terminal fragment N(TW) and a N-terminal fragment N(EC). Following
CC ligand binding, it is cleaved by TNF-alpha converting enzyme
CC (TACE) to yield a membrane-associated intermediate fragment called
CC notch extracellular truncation (NEXT). This fragment is then
CC cleaved by presenilin dependent gamma-secretase to release a

```

CC notch-derived peptide containing the intracellular domain (NICD)
 CC from the membrane (By similarity).
 CC -1- PTM: Phosphorylated (By similarity).
 CC -1- DISEASE: Notch1 truncation is associated with neoplasia, a T-cell
 CC acute lymphoblastic leukemia.
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
 CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
 CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF308602; AAC33848.1; -.
 CC EMBL: M73980; AAA60614.1; -.
 CC HSSP: P00740; 1EDM.
 CC Genew: HGNC:7881; NOTCH1.
 CC MIM: 190198; -.
 CC InterPro: IPR002110; ANK.
 CC InterPro: IPR000152; Asx_hydroxyl.
 CC InterPro: IPR000561; EGF-1like.
 CC InterPro: IPR000742; EGF_2.
 CC InterPro: IPR001881; EGF_Ca.
 CC InterPro: IPR001438; EGF_II.
 CC InterPro: IPR000800; Notch.
 CC Pfam: PF00008; EGF; 36.
 CC Pfam: PF00023; ank; 6.
 CC Pfam: PF00066; notch; 3.
 CC SMART: SM00248; ANK; 5.
 CC SMART: SM00179; EGF_CA; 22.
 CC SMART: SM00001; EGF_1like; 13.
 CC SMART: SM00004; NL; 2.
 CC PROSITE: PS50088; ANK_REPEAT; 4.
 CC PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 CC PROSITE: PS00010; ASX_HYDROXYL; 20.
 CC PROSITE: PS00022; EGF_1; 34.
 CC PROSITE: PS01186; EGF_2; 26.
 CC PROSITE: PS01187; EGF_CA; 18.
 CC Receptor: Transcription regulation; Activator; Differentiation;
 CC Developmental protein; Repeat; ANK repeat; EGF-like domain;
 CC Transmembrane; Glycoprotein; Signal; Phosphorylation.
 CC SIGNAL: 1
 CC CHAIN: 19 2556
 CC CHAIN: 1722 2556
 CC CHAIN: 1755 2556
 CC DOMAIN: 19 1736
 CC TRANSMEM: 1737 1757
 CC DOMAIN: 1758 2556
 CC DOMAIN: 20 58
 CC DOMAIN: 59 99
 CC DOMAIN: 102 139
 CC DOMAIN: 140 176
 CC DOMAIN: 178 216
 CC DOMAIN: 218 255
 CC DOMAIN: 257 293
 CC DOMAIN: 295 333
 CC DOMAIN: 335 371
 CC DOMAIN: 372 410
 CC DOMAIN: 412 450
 CC DOMAIN: 452 488
 CC DOMAIN: 490 526
 CC DOMAIN: 528 564
 CC DOMAIN: 566 601
 CC DOMAIN: 603 639
 CC DOMAIN: 641 676
 CC DOMAIN: 678 714

FT DOMAIN 716 751 EGF-LIKE 19, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 753 789 EGF-LIKE 20.
 FT DOMAIN 791 829 EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 829 868 EGF-LIKE 22.
 FT DOMAIN 870 906 EGF-LIKE 23, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 908 944 EGF-LIKE 24.
 FT DOMAIN 946 982 EGF-LIKE 25, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 984 1020 EGF-LIKE 26.
 FT DOMAIN 1022 1058 EGF-LIKE 27.
 FT DOMAIN 1060 1096 EGF-LIKE 28.
 FT DOMAIN 1098 1144 EGF-LIKE 29.
 FT DOMAIN 1146 1182 EGF-LIKE 30.
 FT DOMAIN 1184 1220 EGF-LIKE 31, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1222 1266 EGF-LIKE 32, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1268 1306 EGF-LIKE 33.
 FT DOMAIN 1308 1347 EGF-LIKE 34.
 FT DOMAIN 1349 1385 EGF-LIKE 35.
 FT DOMAIN 1388 1427 EGF-LIKE 36.
 FT REPEAT 1446 1481 LIN/NOTCH 1.
 FT REPEAT 1482 1523 LIN/NOTCH 2.
 FT REPEAT 1524 1563 LIN/NOTCH 3.
 FT REPEAT 1563 1597 ANK 1.
 FT REPEAT 1597 1631 ANK 2.
 FT REPEAT 1631 1665 ANK 3.
 FT REPEAT 1665 1699 ANK 4.
 FT REPEAT 1699 1732 ANK 5.
 FT DOMAIN 1732 1765 POLY-VAL.
 FT DOMAIN 1765 1799 POLY-ARG.
 FT DOMAIN 1799 1832 POLY-PRO.
 FT DOMAIN 1832 1865 POLY-ALA.
 FT DOMAIN 1865 1898 POLY-GLU.
 FT DOMAIN 1898 1931 POLY-GLY.
 FT DOMAIN 1931 1964 POLY-GLN.
 FT DOMAIN 1964 1997 POLY-PRO.
 FT DOMAIN 1997 2030 POLY-SER.
 FT SITE 2030 2063 CLEAVAGE BY FURIN-LIKE PROTEASE (BY
 FT 1665 SIMILARITY).
 FT DISULFID 24 37 BY SIMILARITY.
 FT DISULFID 31 46 BY SIMILARITY.
 FT DISULFID 48 57 BY SIMILARITY.
 FT DISULFID 63 74 BY SIMILARITY.
 FT DISULFID 87 98 BY SIMILARITY.
 FT DISULFID 106 117 BY SIMILARITY.
 FT DISULFID 111 127 BY SIMILARITY.
 FT DISULFID 129 138 BY SIMILARITY.
 FT DISULFID 144 155 BY SIMILARITY.
 FT DISULFID 149 164 BY SIMILARITY.
 FT DISULFID 166 175 BY SIMILARITY.
 FT DISULFID 182 195 BY SIMILARITY.
 FT DISULFID 189 204 BY SIMILARITY.
 FT DISULFID 206 215 BY SIMILARITY.
 FT DISULFID 222 233 BY SIMILARITY.
 FT DISULFID 227 243 BY SIMILARITY.
 FT DISULFID 245 254 BY SIMILARITY.
 FT DISULFID 261 272 BY SIMILARITY.
 FT DISULFID 266 281 BY SIMILARITY.
 FT DISULFID 283 292 BY SIMILARITY.
 FT DISULFID 299 312 BY SIMILARITY.
 FT DISULFID 306 321 BY SIMILARITY.
 FT DISULFID 323 332 BY SIMILARITY.
 FT DISULFID 339 350 BY SIMILARITY.
 FT DISULFID 344 359 BY SIMILARITY.
 FT DISULFID 361 370 BY SIMILARITY.
 FT DISULFID 376 387 BY SIMILARITY.
 FT DISULFID 381 398 BY SIMILARITY.

Query Match 37.1%; Score 52; DB 1; Length 2556;
 Best Local Similarity 36.4%; Pred. No. 9.8;
 Matches 8; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
 QY 6 QKCFQHLDDCCSXKXCNXNXCXV 27
 | | : : : | | |

Db 252 QNCEMINDCPGNCKNGACV 273

RESULT 10

ID	DL3_RAT	STANDARD	PRT	589 AA.
AC	088671			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Delta-like protein 3 precursor (Drosophila Delta homolog 3).			
GN	DL3			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RP	SEQUENCE FROM N.A.			
RA	Boulter J., Greenfield A., Weinmaster G.;			
RT	"Rattus norvegicus mRNA for Delta 3: a putative ligand for Notch.";			
RL	Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.			
CC	- FUNCTION: INHIBITS PRIMARY NEUROGENESIS. MAY BE REQUIRED TO DIVERGENT NEURONS ALONG A SPECIFIC DIFFERENTIATION PATHWAY. PLAY A ROLE IN THE FORMATION OF SOMITE BOUNDARIES DURING SEGMENTATION OF THE PARAXIAL MESODERM (BY SIMILARITY).			
CC	- SUBUNIT: CAN BIND AND ACTIVATE NOTCH-1 OR ANOTHER NOTCH RECEPTOR (BY SIMILARITY).			
CC	- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).			
CC	- DOMAIN: THE DSL DOMAIN IS REQUIRED FOR BINDING TO THE NOTCH RECEPTOR.			
CC	- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.			
CC	- SIMILARITY: CONTAINS 1 DSL DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL: AF084576; AAC33303.1; -			
DR	HSSP: P00740; 1EDM			
DR	InterPro: IPR000561; EGF-like.			
DR	InterPro: IPR000742; EGF_2.			
DR	InterPro: IPR001881; EGF_Ca.			
DR	Pfam: PF00008; EGF_5.			
DR	SMART: SM00181; EGF: 6.			
DR	PROSITE: PS00022; EGF_1; 6.			
DR	PROSITE: PS01186; EGF_2; 5.			
KW	Signal; EGF-like domain; Repeat; Transmembrane; Developmental protein; Differentiation.			
KW	SIGNAL			
FT	CHAIN	33	589	BY SIMILARITY.
FT	DOMAIN	33	494	DELTA-LIKE PROTEIN 3.
FT	TRANSMEM	495	515	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	516	589	POTENTIAL.
FT	DOMAIN	174	213	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	218	251	DSL.
FT	DOMAIN	276	312	EGF-LIKE 1.
FT	DOMAIN	314	353	EGF-LIKE 2.
FT	DOMAIN	355	391	EGF-LIKE 3.
FT	DOMAIN	393	429	EGF-LIKE 4.
FT	DOMAIN	431	467	EGF-LIKE 5.
FT	DOMAIN	503	511	EGF-LIKE 6.
FT	DOMAIN	511	589	POLY-ALA.
FT	DISULFID	222	233	BY SIMILARITY.
FT	DISULFID	226	239	BY SIMILARITY.
FT	DISULFID	241	250	BY SIMILARITY.
FT	DISULFID	280	291	BY SIMILARITY.
FT	DISULFID	285	300	BY SIMILARITY.
FT	DISULFID	302	311	BY SIMILARITY.
FT	DISULFID	318	329	BY SIMILARITY.
FT	DISULFID	323	341	BY SIMILARITY.

Query Match 36.4%; Score 51; DB 1; Length 589;
Best Local Similarity 34.5%; Pred. No. 4.1;
Matches 10; Conservative 1; Mismatches 16; Indels 2; Gaps 1;

QY 1 CR-1XNKCFOHLDCCSXXCNXNKCXV 27

Db 381 CRAGFAGPRCEHDDDCAGACNGCTCV 409

RESULT 11

ID	DL3_MOUSE	STANDARD	PRT	592 AA.
AC	088516; Q9QW27; Q35675; Q9QWL9;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Delta-like protein 3 precursor (Drosophila Delta homolog 3) (M-Delta-3).			
DE	Delta-like protein 3 precursor (Drosophila Delta homolog 3) (M-Delta-3).			
GN	DL3			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	STRAIN=C57BL/6 X DBA; TISSUE=Embryo;			
RC	MEDLINE=96324780; PubMed=9662403;			
RX	Kusumi K., Sun E.S., Kerrebrock A.W., Bronson R.T., Chi D.-C.,			
RA	Bulotsky M.S., Spencer J.B., Birren B.W., Frankel W.N., Lander E.S.;			
RT	"The mouse pudgy mutation disrupts Delta homologue Dll3 and initiation of early somite boundaries.";			
RT	Nat. Genet. 19:274-278(1998).			
RL	[3]			
RN	SEQUENCE FROM N.A. (ISOFORM 1).			
RP	TISSUE-Neural tube;			
RC	"Specific expression of a divergent type of Delta in a set of earliest generated neurons including the prospective subplate neurons.";			
RT	Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.			
RL	FUNCTION: INHIBITS PRIMARY NEUROGENESIS. MAY BE REQUIRED TO DIVERGENT NEURONS ALONG A SPECIFIC DIFFERENTIATION PATHWAY. PLAY A ROLE IN THE FORMATION OF SOMITE BOUNDARIES DURING SEGMENTATION OF THE PARAXIAL MESODERM.			
CC	- SUBUNIT: CAN BIND AND ACTIVATE NOTCH-1 OR ANOTHER NOTCH RECEPTOR (PROBABLY).			
CC	- SUBCELLULAR LOCATION: Type I membrane protein (Probable).			
CC	- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 AND 2 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE NEUROECTODERM AND PARAXIAL MESODERM DURING EMBRYOGENESIS.			
CC	- DOMAIN: THE DSL DOMAIN IS REQUIRED FOR BINDING TO THE NOTCH RECEPTOR.			

CC -1- DISEASE: A TRUNCATING MUTATION IN DLL3 IS THE CAUSE OF THE PUDGY
 CC (PU) PHENOTYPE. PUDGY MICE EXHIBIT PATTERNING DEFECTS AT THE
 CC EARLIEST STAGES OF SOMITOGENESIS. ADULT PUDGY MICE PRESENT SEVERE
 CC VERTEBRAL AND RIB DEFORMITIES.
 CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: AF068665; AAC40170.1; -
 DR EMBL: AF068665; AAC40169.1; -
 DR EMBL: Y11895; CAAT72637.1; -
 DR EMBL: AB013440; BAA3716.1; -
 DR HSSP: P00740; 1EDM.
 DR MGD: MGI:1096877; D113.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_II.
 DR Pfam: PF00008; EGF; 5.
 DR PRINTS: PR00010; EGFBL00D.
 DR SMART: SM00181; EGF; 6.
 DR PROSITE: PS00022; EGF_1; 6.
 DR PROSITE: PS01186; EGF_2; 6.
 DR Signal: EGF-like domain; Repeat; Transmembrane; Developmental protein;
 DR KW Differential: Alternative splicing.
 FT SIGNAL 1 32
 FT CHAIN 33 592
 FT DOMAIN 33 490
 FT TRANSLEM 491 511
 FT DOMAIN 512 592
 FT DOMAIN 174 213
 FT DOMAIN 214 247
 FT DOMAIN 272 308
 FT DOMAIN 310 349
 FT DOMAIN 351 387
 FT DOMAIN 389 425
 FT DOMAIN 427 463
 FT DOMAIN 218 229
 FT DISULFID 222 235
 FT DISULFID 237 246
 FT DISULFID 276 287
 FT DISULFID 281 296
 FT DISULFID 298 307
 FT DISULFID 314 325
 FT DISULFID 319 337
 FT DISULFID 339 348
 FT DISULFID 355 366
 FT DISULFID 360 375
 FT DISULFID 377 386
 FT DISULFID 393 404
 FT DISULFID 398 413
 FT DISULFID 415 424
 FT DISULFID 431 442
 FT DISULFID 436 451
 FT DISULFID 453 462
 FT VARSPLIC 585 592
 FT CONFLICT 94 94
 FT CONFLICT 401 401
 FT SEQUENCE 592 AA; 62069 MW; 1A84F8022E7EDCC CRC64;
 Query Match 36.4%; Score 51; DB 1; Length 592;
 Best Local Similarity 34.5%; Pred. No. 4.1;
 Matches 10; Conservative 1; Mismatches 16; Indels 2; Gaps 1;

DB 377 CRAGFAGPRCEHDDCCACRACANGTCV 405
 RESULT 12
 ID DLL3_HUMAN STANDARD; PRT; 618 AA.
 AC 09NYJ7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Delta-like protein 3 precursor (Drosophila Delta homolog 3).
 GN DLL3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT SD ASP-385.
 RX MEDLINE=20206573; PubMed=10742114;
 RA Bulman M.P., Kusumi K., Frayling T.M., McKewen C., Garrett C.,
 RA Lander E.S., Krumlauf R., Hattersley A.T., Ellard S., Turnpenny P.D.,
 RT "Mutations in the human delta homologue, DLL3, cause axial skeletal
 RT defects in spondylocostal dysostosis.";
 RL Nat. Genet. 24:438-441(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INHIBITS PRIMARY NEUROGENESIS. MAY BE REQUIRED TO DIVERT
 CC NEURONS ALONG A SPECIFIC DIFFERENTIATION PATHWAY. PLAY A ROLE IN
 CC THE FORMATION OF SOMITE BOUNDARIES DURING SEGMENTATION OF THE
 CC PARAXIAL MESODERM (BY SIMILARITY).
 CC -1- SUBUNIT: CAN BIND AND ACTIVATE NOTCH-1 OR ANOTHER NOTCH RECEPTOR
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
 CC -1- DOMAIN: THE DSL DOMAIN IS REQUIRED FOR BINDING TO THE NOTCH
 CC RECEPTOR.
 CC -1- DISEASE: DEFECTS IN DLL3 ARE A CAUSE OF AUTOSOMAL RECESSIVE
 CC SPONDYLOCOSTAL DYSOSTOSIS (SD). IT IS CHARACTERIZED BY MULTIPLE
 CC HEMIVERTEBRAE, RIB FUSIONS AND DELETIONS WITH A NON-PROGRESSIVE
 CC KYPHOSCOLIOSIS.
 CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 DSL DOMAIN.
 CC -----
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 CC -----
 DR EMBL: AF241373; AAF62542.1; -
 DR EMBL: AF241367; AAF62542.1; JOINED.
 DR EMBL: AF241368; AAF62542.1; JOINED.
 DR EMBL: AF241369; AAF62542.1; JOINED.
 DR EMBL: AF241370; AAF62542.1; JOINED.
 DR EMBL: AF241371; AAF62542.1; JOINED.
 DR EMBL: AF241372; AAF62542.1; JOINED.
 DR EMBL: BC000218; AAH00218.1; -
 DR HSSP: P00740; 1EDM.
 DR Genew: HGNC:2909; DLL3.
 DR MIM: 602768; -
 DR MIM: 277300; -
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_II.
 DR Pfam: PF00008; EGF; 5.
 DR PRINTS: PR00010; EGFBL00D.
 DR SMART: SM00181; EGF; 6.
 DR PROSITE: PS00022; EGF_1; 6.

DR PROSITE: PS01186; EGF_2; 6.
 KW Signal; EGF-like domain; Repeat; Transmembrane; Developmental protein;
 KW Differentiation; Disease mutation.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 618 DELTA-LIKE PROTEIN 3.
 FT DOMAIN 27 492 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 493 513 POTENTIAL.
 FT DOMAIN 514 618 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 176 215 DSL.
 FT DOMAIN 176 215 EGF-LIKE 1.
 FT DOMAIN 274 310 EGF-LIKE 2.
 FT DOMAIN 312 351 EGF-LIKE 3.
 FT DOMAIN 353 389 EGF-LIKE 4.
 FT DOMAIN 391 427 EGF-LIKE 5.
 FT DOMAIN 429 465 EGF-LIKE 6.
 FT DISULFID 220 231 BY SIMILARITY.
 FT DISULFID 224 237 BY SIMILARITY.
 FT DISULFID 239 248 BY SIMILARITY.
 FT DISULFID 278 289 BY SIMILARITY.
 FT DISULFID 283 298 BY SIMILARITY.
 FT DISULFID 300 309 BY SIMILARITY.
 FT DISULFID 316 327 BY SIMILARITY.
 FT DISULFID 321 339 BY SIMILARITY.
 FT DISULFID 341 350 BY SIMILARITY.
 FT DISULFID 357 368 BY SIMILARITY.
 FT DISULFID 362 377 BY SIMILARITY.
 FT DISULFID 379 388 BY SIMILARITY.
 FT DISULFID 395 406 BY SIMILARITY.
 FT DISULFID 400 415 BY SIMILARITY.
 FT DISULFID 417 426 BY SIMILARITY.
 FT DISULFID 433 444 BY SIMILARITY.
 FT DISULFID 438 453 BY SIMILARITY.
 FT DISULFID 455 464 BY SIMILARITY.
 FT VARIANT 385 385 G -> D (IN SD).
 FT VARIANT 385 385 /FTID-VAR-009952.
 SQ SEQUENCE 618 AA; 64617 MW; 58AB9CA7DEAD1A0 CRC64;
 Query Match 36.4%; Score 51; DB 1; Length 618;
 Best Local Similarity 34.5%; Pred. No. 4.3;
 Matches 10; Conservative 1; Mismatches 16; Indels 2; Gaps 1;
 QY 1 CR--IXNKKCFQHDCCSXXCNXNCV 27
 Db 379 CRAFGAPRCEHDLDDCAGRCANGGCV 407
 RESULT 13
 NTC4_HUMAN STANDARD; PRT; 2003 AA.
 AC 099466; 000306; 099940; 099458; 099358; 090119; 090110;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neogenetic locus notch homolog protein 4 precursor (Notch 4)
 DE (hnotch4).
 GN NOTCH4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND POLYMORPHISM OF POLY-LEU.
 RC TISSUE=Placenta;
 RX MEDLINE=97311416; PubMed=9168133;
 RA Sugaya K., Saenunuma S.-I., Nohata J., Kimura T., Fukagawa T.,
 RA Nakamura Y., Ando A., Inoko H., Ikemura T., Mita K.;
 RT "Gene organization of human NOTCH4 and (CTG)n polymorphism in this
 RL human counterpart gene of mouse proto-oncogene Int3.";
 RL Gene 189:235-244(1997).
 RN 1
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC TISSUE=Bone marrow; and Heart;
 RX MEDLINE=98360091; PubMed=9693032;

RA Li L., Huang G.M., Banta A.B., Deng Y., Smith T., Dong P.,
 RA Friedman C., Chen L., Trask B.J., Spies T., Rowen L., Hood L.;
 RT "Cloning, characterization, and the complete 56.8-kilobase DNA
 RT sequence of the human NOTCH4 gene.";
 RN Genomics 51:45-58(1998).
 RP SEQUENCE OF 1-503 FROM N.A., AND VARIANTS GLN-117 AND GLN-317.
 RA Miyagawa T., Tokunaga K., Hojo H.;
 RT "Human notch4 gene variant.";
 RN Submitted (Feb-1999) to the EMBL/Genbank/DBJ databases.
 RP IDENTIFICATION OF LIGANDS.
 RX MEDLINE=99180765; PubMed=10079256;
 RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
 RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Aravanis-Tsakonas S.,
 RL "Human ligands of the Notch receptor.";
 CC Am. J. Pathol. 154:785-794(1999).
 CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands
 CC jagged1, jagged2 and delta1 to regulate cell-fate determination.
 CC Upon ligand activation through the released notch intracellular
 CC domain (NICD) it forms a transcriptional activator complex with
 CC RBP-J kappa and activates genes of the enhancer of split locus.
 CC Affects the implementation of differentiation, proliferation and
 CC apoptotic programs. May regulate branching morphogenesis in the
 CC developing vascular system (By similarity).
 CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
 CC terminal fragment N(TEC) which are probably linked by disulfide
 CC bonds (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following
 CC proteolytical processing NICD is translocated to the nucleus.
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms, 1 (shown here), 2 and 3; may be
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Highly expressed
 CC in the lung and placenta and at low levels in the liver, skeletal
 CC muscle, kidney, pancreas, spleen, lymph node, thymus, bone marrow
 CC and fetal liver. No expression was seen in adult brain or
 CC peripheral blood leukocytes.
 CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form
 CC which is proteolytically cleaved by a furin-like convertase in the
 CC trans-golgi network before it reaches the plasma membrane to yield
 CC an active, ligand-accessible form. Cleavage results in a C-
 CC terminal fragment N(TM) and a N-terminal fragment N(TEC). Following
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme
 CC (TACE) to yield a membrane-associated intermediate fragment called
 CC notch extracellular truncation (NEXT). This fragment is then
 CC cleaved by presenilin dependent gamma-secretase to release a
 CC notch-derived peptide containing the intracellular domain (NICD)
 CC from the membrane (By similarity).
 CC -1- PTM: Phosphorylated (By similarity).
 CC -1- POLYMORPHISM: The poly-leu region of NOTCH4 (in the signal
 CC peptide) is polymorphic and the number of leu varies in the
 CC population (from 6 to 12).
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
 CC -1- SIMILARITY: CONTAINS 28 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
 CC in position 1438 to 1463.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, D63395; BA09708.1; ALT_FRAME.
 DR EMBL, D86566; BA013116.1; -
 DR EMBL, U95299; AAC32288.1; -
 DR EMBL, U89335; AAC63097.1; -
 DR EMBL, AB023961; BAB20317.1; -
 DR EMBL, AB024520; BAB88951.1; -

DR EMBL; AB024578; BAA8952.1; -
 DR HSSP; P08709; 1BF9.
 DR Genew; HGNC:7884; NOTCH4.
 DR MIM; 164951; -
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF-II.
 DR InterPro; IPR000800; Notch.
 DR Pfam; PF00008; EGF; 26.
 DR Pfam; PF00023; ank; 6.
 DR Pfam; PF00066; notch; 2.
 DR PRINTS; PR00010; EGFBL00.
 DR PRINTS; PR00011; EGFLEMININ.
 DR PRINTS; PR00012; ENTPEI.
 DR SMART; SM00248; ANK; 5.
 DR SMART; SM00179; EGF_CA; 11.
 DR SMART; SM00001; EGF-like; 15.
 DR SMART; SM00004; NL; 2.
 DR PROSITE; PSS0008; ANK_REPEAT; 5.
 DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PSS0010; ASX_HYDROXYL; 11.
 DR PROSITE; PSS00022; EGF_1; 28.
 DR PROSITE; PSS0186; EGF_2; 21.
 DR PROSITE; PSS0187; EGF_CA; 9.
 KW Receptor: Transcription regulation; Activator; Differentiation;
 KW Developmental protein: Repeat: ANK repeat: EGF-like domain;
 KW Transmembrane; Glycoprotein; Signal; Phosphorylation; Polymorphism;
 KW Triplet repeat expansion; Alternative splicing.
 FT SIGNAL 1 23
 FT CHAIN 24 2003
 FT CHAIN 1432 2003
 FT CHAIN 1467 2003
 FT CHAIN 1467 2003
 FT DOMAIN 24 1447
 FT TRANSMEM 1448 1468
 FT DOMAIN 1469 2003
 FT DOMAIN 24 63
 FT DOMAIN 64 115
 FT DOMAIN 118 155
 FT DOMAIN 156 192
 FT DOMAIN 194 232
 FT DOMAIN 234 274
 FT DOMAIN 276 312
 FT DOMAIN 314 353
 FT DOMAIN 355 391
 FT DOMAIN 392 430
 FT DOMAIN 432 473
 FT DOMAIN 475 511
 FT DOMAIN 513 549
 FT DOMAIN 551 587
 FT DOMAIN 589 625
 FT DOMAIN 626 659
 FT DOMAIN 661 689
 FT DOMAIN 691 727
 FT DOMAIN 729 765
 FT DOMAIN 767 803
 FT DOMAIN 806 842
 FT DOMAIN 844 880
 FT DOMAIN 882 928
 FT DOMAIN 930 966
 FT DOMAIN 968 1004
 FT DOMAIN 1006 1044
 FT DOMAIN 1046 1085
 FT DOMAIN 1087 1126
 FT DOMAIN 1130 1171
 FT DOMAIN 1173 1212
 FT REPEAT 1213 1246
 FT REPEAT 1247 1286

FT REPEAT 1633 1665 ANK 1.
 FT REPEAT 1666 1698 ANK 2.
 FT REPEAT 1700 1732 ANK 3.
 FT REPEAT 1733 1765 ANK 4.
 FT REPEAT 1766 1798 ANK 5.
 FT DISULFID 28 41
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 FT DISULFID 105 114
 FT DISULFID 122 133
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 FT DISULFID 145 154
 FT DISULFID 160 171
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 FT DISULFID 182 191
 FT DISULFID 198 211
 FT DISULFID 205 220
 FT DISULFID 222 231
 FT DISULFID 238 249
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 FT DISULFID 302 311
 FT DISULFID 318 332
 FT DISULFID 326 341
 FT DISULFID 343 352
 Query Match 36.4%; Score 51; DB 1; Length 2003;
 Best Local Similarity 35.0%; Pred. No. 11;
 Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 QY 8 CPOHLDDCCXXKXNKCXV 27
 Db 352 CERNLDDCTAATCAPOSTCT 371
 RESULT 14
 NTCL_MOUSE
 ID NCCL_MOUSE STANDARD; PRT: 2531 AA.
 AC 001705; Q9QW58; Q99JC2; Q06007; Q61905; Q9R0X7;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neurogenic locus notch homolog protein 1 precursor (Notch 1) (Notch A)
 DE (M714) (p300).
 GN NOTCH1 OR NOTCH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Embryo;
 RA MEDLINE=93194170; PubMed=8449489;
 RA Franco del Amo F., Gendron-Maguire M., Swiatek P.D., Jenkins N.A.,
 RA Copeland N.G., Gridley T.;
 RT "Cloning, analysis, and chromosomal localization of Notch-1, a mouse
 RT homolog of Drosophila Notch.";
 RL Genomics 15:259-264(1993).
 RN [2]
 RP SEQUENCE OF 731-1899 FROM N.A. (ISOFORM 2), AND DEVELOPMENTAL STAGE.
 RC STRAIN=CD-1; TISSUE=Embryo;
 RX MEDLINE=93050801; PubMed=1426644;
 RX Reaume A.G., Conlon R.A., Zingib R., Yamaguchi T.P., Rossant J.;
 RT "Expression analysis of a Notch homologue in the mouse embryo.";
 RL Dev. Biol. 154:377-387(1992).
 RN [3]
 RP SEQUENCE OF 1551-1647 FROM N.A. (ISOFORM 1), AND DEVELOPMENTAL STAGE.
 RC TISSUE=Embryo;
 RX MEDLINE=93048835; PubMed=1425352;

RA Franco del Amo F., Smith D.E., Swiatek P.J., Gendron-Maguire M.,
 RA Greenspan R.J., McMahon A.P., Gridley T.;
 RT "Expression pattern of Notch, a mouse homolog of Drosophila Notch,
 RT suggests an important role in early postimplantation mouse
 RT development.";
 RL Development 115:737-744(1992).
 RN [4]
 RP SEQUENCE OF 1161-1547 FROM N.A.
 RC STRAIN-C57BL/6 X CBA; TISSUE-Embryo;
 RX MEDLINE-93178563; PubMed-8440332;
 RA Lardelli M., Lendahl U.;
 RT "Notch A and Notch B-two mouse Notch homologues coexpressed in a
 RT wide variety of tissues";
 RL Exp. Cell Res. 204:364-372(1993).
 RN [5]
 RP SEQUENCE OF 1659-1673 FROM N.A.
 RX MEDLINE-99364499; PubMed-10437788;
 RA Lee J.S., Ishimoto A., Yanagawa S.I.;
 RT "Murine leukemia provirus-mediated activation of the Notch1 gene leads
 RT to induction of HES-1 in a mouse T lymphoma cell line, DL-3.";
 RL FEBS Lett. 455:276-280(1999).
 RN [6]
 RP SEQUENCE OF 1950-2201 FROM N.A.
 RX MEDLINE-98029496; PubMed-9384671;
 RA Messierle M., Pollo M., Nehls M., Eggert H., Boehm T.;
 RT "Dynamic changes in gene expression during in vitro differentiation of
 RT mouse embryonic stem cells.";
 RL Cytokines Cell. Mol. Ther. 1:139-143(1995).
 RN [7]
 RP SEQUENCE OF 1655-1659, CLEAVAGE BY PURIN-LIKE CONVERTASE, AND
 RP NOTAGENSIS OF 1651-ARG-GLN-ARG-ARG-1654.
 RX MEDLINE-98318619; PubMed-9653148;
 RA Logeat F., Bessia C., Brou C., Lebail O., Jarriault S., Seidah N.G.,
 RA Israel A.;
 RT "The Notch1 receptor is cleaved constitutively by a furin-like
 RT convertase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8108-8112(1998).
 RN [8]
 RP PARTIAL SEQUENCE, AND POST-TRANSLATIONAL PROCESSING.
 RX MEDLINE-21523956; PubMed-11518718;
 RA Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
 RT "Murine notch homologs (NL-4) undergo presenilin-dependent
 RT proteolysis.";
 RL J. Biol. Chem. 276:40268-40273(2001).
 RN [9]
 RP POST-TRANSLATIONAL PROCESSING.
 RX MEDLINE-21374376; PubMed-11459941;
 RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
 RT "Conservation of the biochemical mechanisms of signal transduction
 RT among mammalian Notch family members.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
 CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands
 CC Jagged1, Jagged2 and Delta to regulate cell-fate determination.
 CC Upon ligand activation through the released notch intracellular
 CC domain (NICD) it forms a transcriptional activator complex with
 CC RBP-J kappa and activates genes of the enhancer of split locus.
 CC Affects the implementation of differentiation, proliferation and
 CC apoptotic programs (By similarity). May play an essential role in
 CC postimplantation development, probably in some aspect of cell
 CC specification and/or differentiation. May be involved in mesoderm
 CC development, somite formation and neurogenesis. Involved in the
 CC maturation of both CD4+ and CD8+ cells in the thymus.
 CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
 CC terminal fragment N(EC) which are probably linked by disulfide
 CC bonds.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following
 CC proteolytical processing NICD is translocated to the nucleus.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Highly expressed in the brain, lung and
 CC thymus. Expressed at lower levels in the spleen, bone-marrow,
 CC spinal cord, eyes, mammary gland, liver, intestine, skeletal
 CC muscle, kidney and heart.

CC -1- DEVELOPMENTAL STAGE: First detected in the mesoderm at 7.5 d.p.c.
 CC By 8.5 d.p.c. highly expressed in presomitic mesoderm, mesenchyme
 CC and endothelial cells, while much lower levels are seen in the
 CC neuroepithelium. Between 9.5-10.5 d.p.c. expressed at high levels
 CC in the neuroepithelium. At 13.5 d.p.c. expressed in the surface
 CC ectoderm, eye and developing whisker follicles.
 CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form
 CC which is proteolytically cleaved by a furin-like convertase in the
 CC trans-Golgi network before it reaches the plasma membrane to yield
 CC an active, ligand-accessible form. Cleavage results in a C-
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme
 CC (TACE) to yield a membrane-associated intermediate fragment called
 CC notch extracellular truncation (NEXT). This fragment is then
 CC cleaved by presenilin dependent gamma-secretase to release a
 CC notch-derived peptide containing the intracellular domain (NICD)
 CC from the membrane.
 CC -1- PTM: Phosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
 CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
 CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Z11886; CAA77941.1; -
 CC EMBL: L02613; AAK14898.1; -
 CC EMBL: X68278; CAA48339.1; -
 CC EMBL: AJ238029; CAA40733.1; -
 CC EMBL: X82562; CAA57909.1; -
 CC HSP: P00740; IEDM.
 CC MGD: MGI:97363; Notch1.
 CC InterPro: IPR002110; ANK.
 CC InterPro: IPR000152; Asx_hydroxyl.
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR007442; EGF-2.
 CC InterPro: IPR001881; EGF_CA.
 CC InterPro: IPR001438; EGF_11.
 CC InterPro: IPR000800; Notch.
 CC Pfam: PF00008; EGF; 35.
 CC Pfam: PF00023; ank; 7.
 CC Pfam: PF00066; notch; 3.
 CC PRINTS: PR00010; EGFBLDOD.
 CC PRINTS: PR01452; NOTCH.
 CC SMART: SM00248; ANK; 3.
 CC SMART: SM00179; EGF_CA; 23.
 CC SMART: SM00001; EGF-like; 11.
 CC SMART: SM00004; NL; 2.
 CC PROSITE: PS50088; ANK_REPEAT; 2.
 CC PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 CC PROSITE: PS00010; ASX_HYDROXYL; 22.
 CC PROSITE: PS00022; EGF_1; 34.
 CC PROSITE: PS01186; EGF-2; 27.
 CC PROSITE: PS01187; EGF_CA; 21.
 CC Receptor; Transcription regulation; Activator; Differentiation;
 CC Developmental protein; Repeat; ANK repeat; EGF-like domain;
 CC Transmembrane; Glycoprotein; Signal; Phosphorylation;
 CC Alternative splicing.
 CC SIGNAL 18
 CC CHAIN 19 2531 POTENTIAL.
 CC CHAIN 1711 2531 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1.
 CC CHAIN 1744 2531 NOTCH EXTRACELLULAR TRUNCATION.
 CC CHAIN 19 1725 NOTCH INTRACELLULAR DOMAIN.
 CC TRANSMM 1726 1746 EXTRACELLULAR (POTENTIAL).
 CC TRANSMM 1747 2531 POTENTIAL.
 CC DOMAIN 20 58 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 59 99 EGF-LIKE 1.
 CC DOMAIN 59 99 EGF-LIKE 2.

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FT DOMAIN 102 139 EGF-LIKE 3.
FT DOMAIN 140 176 EGF-LIKE 4.
FT DOMAIN 178 216 EGF-LIKE 5.
FT DOMAIN 218 255 EGF-LIKE 6.
FT DOMAIN 257 293 EGF-LIKE 7.
FT DOMAIN 295 333 EGF-LIKE 8.
FT DOMAIN 335 371 EGF-LIKE 9.
FT DOMAIN 372 410 EGF-LIKE 10.
FT DOMAIN 412 450 EGF-LIKE 11.
FT DOMAIN 452 488 EGF-LIKE 12.
FT DOMAIN 490 526 EGF-LIKE 13.
FT DOMAIN 528 564 EGF-LIKE 14.
FT DOMAIN 566 601 EGF-LIKE 15.
FT DOMAIN 603 639 EGF-LIKE 16.
FT DOMAIN 641 676 EGF-LIKE 17.
FT DOMAIN 678 714 EGF-LIKE 18.
FT DOMAIN 716 751 EGF-LIKE 19.
FT DOMAIN 753 789 EGF-LIKE 20.
FT DOMAIN 791 827 EGF-LIKE 21.
FT DOMAIN 829 867 EGF-LIKE 22.
FT DOMAIN 869 905 EGF-LIKE 23.
FT DOMAIN 907 943 EGF-LIKE 24.

Query Match 36.4%; Score 51; DB 1; Length 2531;
Best Local Similarity 36.4%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 6 QKCFQHLDDCCSXKXNXCVCV 27
DB 252 QNCEENVDCCGNNCKNGACV 273

RESULT 15
ID NCCL RAT STANDARD; PRT; 2531 AA.
AC 007008:
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurogenic locus notch homolog protein 1 precursor (Notch 1).
GN NOTCH1.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
ON (1)
RP SEQUENCE FROM N.A.
RC TISSUE-Schwann cell;
RX MEDLINE=92111383; PubMed=1764995;
RA Weinmaster G., Roberts V.J., Lemke G.;
RT "A homolog of Drosophila Notch expressed during mammalian
RT development.";
RL Development 113:199-205(1991).
RN (2)
RN REVISIONS TO 1652-1653.
RA Weinmaster G.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN (3)
RP FUNCTION.
RX MEDLINE=21094508; PubMed=11182080;
RA Tanigaki K., Nogaki F., Takahashi J., Tashiro K., Kurooka H.,
RA Honjo T.;
RT "Notch1 and Notch3 instructively restrict bFGF-responsive multipotent
RT neural progenitor cells to an astroglial fate.";
RL Neuron 29:45-55(2001).
RN (4)
RP TISSUE SPECIFICITY.
RX MEDLINE=93202015; PubMed=1295745;
RA Weinmaster G., Roberts V.J., Lemke G.;
RT "Notch2: a second mammalian Notch gene.";
RL Development 116:931-941(1992).
RN (5)
RP TISSUE SPECIFICITY.

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RX MEDLINE=21331789; PubMed=11438922;
RA Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.;
RT "Expression patterns of Notch1, Notch2, and Notch3 suggest multiple
RT functional roles for the Notch-DSL signaling system during brain
RT development.";
RL J. Comp. Neurol. 436:167-181(2001).
CC
CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands
CC jagged1, jagged2 and Delta1 to regulate cell-fate determination.
CC Upon ligand activation through the released notch intracellular
CC domain (NICD) it forms a transcriptional activator complex with
CC RBP-J kappa and activates genes of the enhancer of split locus.
CC Affects the implementation of differentiation, proliferation and
CC apoptotic programs (By similarity). Acts instructively to control
CC the cell fate determination of CNS multipotent progenitor cells,
CC resulting in astroglial induction and neuron/oligodendrocyte
CC suppression.
CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
CC terminal fragment N(EC) which are probably linked by disulfide
CC bonds (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following
CC proteolytical processing NICD is translocated to the nucleus (By
CC similarity).
CC -1- TISSUE SPECIFICITY: Expressed in the brain, kidney and spleen.
CC Expressed in postnatal central nervous system (CNS) germinal zones
CC and, in early postnatal life, within numerous cells throughout the
CC CNS. Found in both subventricular and ventricular germinal zones.
CC -1- DEVELOPMENTAL STAGE: In the embryo, highest levels occur between
CC days 12 and 14 and decrease rapidly to much lower levels in the
CC adult.
CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form
CC which is proteolytically cleaved by a furin-like convertase in the
CC trans-Golgi network before it reaches the plasma membrane to yield
CC an active, ligand-accessible form. Cleavage results in a C-
CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following
CC ligand binding, it is cleaved by TNF-alpha converting enzyme
CC (TACE) to yield a membrane-associated intermediate fragment called
CC notch extracellular truncation (NEXT). This fragment is then
CC cleaved by presenilin dependent gamma-secretase to release a
CC notch-derived peptide containing the intracellular domain (NICD)
CC from the membrane (By similarity).
CC -1- PTM: Phosphorylated (By similarity).
CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.
CC
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CC -----
CC EMBL: X57405; CAA40667.1; -.
CC HSSP: P00740; IEDM.
CC DR InterPro: IPR002110; ANK.
CC DR InterPro: IPR000152; Asx_hydroxyl.
CC DR InterPro: IPR000561; EGF-like.
CC DR InterPro: IPR000742; EGF-2.
CC DR InterPro: IPR001881; EGF-Ca.
CC DR InterPro: IPR001438; EGF-IT.
CC DR InterPro: IPR002049; Laminin_EGF.
CC DR InterPro: IPR000800; Notch.
CC DR Pfam: PF00008; EGF_36.
CC DR Pfam: PF00023; ank_6.
CC DR Pfam: PF00066; notch_3.
CC DR PRINTS: PR00010; EGFBL00D.
CC DR PRINTS: PR00011; EGFBLAMIN.
CC DR PRINTS: PR01452; NOTCH.
CC DR SMART: SM00248; ANK_5.
CC DR SMART: SM00179; EGF_CA_25.
CC DR SMART: SM00001; EGF_Like_10.

```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 18:26:16 ; Search time 29 Seconds

(without alignments)
191.837 Million cell updates/sec

Title: US-09-666-837B-1-COPY

Perfect score: 140

Sequence: 1 CRIYNQKcFQhLDCCSXKXKXKXCV 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	40.0	752	13	042374 brachydanio
2	55	39.3	664	13	091AT6
3	53	37.9	1685	5	09U4A2
4	52	37.1	642	13	P79941
5	52	37.1	2447	13	P79941 xenopus lae
6	51	36.4	1214	13	013149
7	50	35.7	244	5	09VSG1
8	50	35.7	354	5	09XV21
9	50	35.7	2653	5	025253
10	49	35.0	358	10	091P7
11	49	35.0	721	13	021902
12	49	35.0	1440	5	020204
13	49	35.0	2352	5	061240
14	49	35.0	3623	11	070244
15	48.5	34.6	1208	5	023456
16	48	34.3	448	5	026107

17	48	34.3	552	5	045117	045117 chironomus
18	48	34.3	1075	5	09NC90	09NC90 strongyloce
19	48	34.3	1372	5	P91526	P91526 caenorhabdi
20	48	34.3	2146	5	09VC97	09VC97 drosophila
21	48	34.3	2531	5	016004	016004 lytechinus
22	47.5	33.9	53	12	089743	089743 buzura supp
23	47.5	33.9	53	12	091MH9	091MH9 lymantiria d
24	47	33.6	346	2	08VUT4	08VUT4 pseudomonas
25	47	33.6	464	5	095RM9	095RM9 drosophila
26	47	33.6	530	5	024526	024526 drosophila
27	47	33.6	615	13	057409	057409 brachydanio
28	47	33.6	723	4	09UUT2	09UUT2 homo sapien
29	47	33.6	723	4	09N041	09N041 homo sapien
30	47	33.6	1216	13	090V55	090V55 brachydanio
31	47	33.6	1254	13	09YHU2	09YHU2 brachydanio
32	47	33.6	1254	13	090V56	090V56 brachydanio
33	47	33.6	1290	13	09M6E1	09M6E1 gallus gall
34	47	33.6	1316	4	086UT7	086UT7 homo sapien
35	47	33.6	1480	5	09VTF8	09VTF8 drosophila
36	47	33.6	1504	5	09XVY4	09XVY4 drosophila
37	47	33.6	1504	5	09V7P9	09V7P9 drosophila
38	47	33.6	1551	5	09NGV4	09NGV4 drosophila
39	47	33.6	3396	5	09VM55	09VM55 drosophila
40	46.5	33.2	69	5	09UA92	09UA92 conus abbre
41	46.5	33.2	69	5	09TVK4	09TVK4 conus abbre
42	46.5	33.2	69	5	09TVK3	09TVK3 conus abbre
43	46	32.9	778	13	091BG4	091BG4 xenopus lae
44	46	32.9	1687	11	061204	061204 mus muscucu
45	46	32.9	2524	5	09GPA5	09GPA5 branchiosto

ALIGNMENTS

RESULT 1
ID 042374 PRELIMINARY; PRT; 752 AA.
AC 042374;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Notch receptor protein (Fragment).
GN NOTCH2 OR NOTCH6.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Westlin J., Lardelli M.;
RT "Three novel Notch genes in zebrafish: implications for vertebrate
RT Notch gene evolution and function.";
RL Dev. Genes Evol. 207:51-63(1997).
DR EMBL; Y10354; CAA71380.1; -;
DR HSSP; P00740; IEDM.
DR ZFIN; ZDB-GENE-000329-4; notch2.
DR InterPro; IPR000152; ASX_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_IT.
DR InterPro; IPR000083; Fibrinctn.
DR InterPro; IPR002049; Laminln_EGF.
DR InterPro; IPR000800; Notch.
DR Pfam; PF00008; EGF; 16.
DR Pfam; PF00066; notch; 2.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00011; EGFGLAMININ.
DR PRINTS; PR00012; FNTYPEP.
DR SMART; SM00179; EGF_Ca; 9.
DR SMART; SM00001; EGF_Like; 5.
DR SMART; SM00004; NL; 2.

DR PROSITE; PS00010; ASX_HYDROXYL; 22.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_34.
 DR PROSITE; PS01186; EGF_2; 28.
 DR PROSITE; PS01187; EGF_CA; 21.
 KW ANK repeat; Calcium-binding; EGF-like domain; Glycoprotein;
 KW Hydroxylation; Repeat.
 SO SEQUENCE 2653 AA; 285928 MW; 6AF2A058FE6C329 CRC64;
 Query Match 35.7%; Score 50; DB 5; Length 2653;
 Best Local Similarity 31.8%; Pred. No. 12;
 Matches 7; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
 Db 270 KNCBQNDIDCGHLCONGGTCT 291
 QY 6 QKCFQHLDDCCSXCNXNXC 27
 RESULT 10
 ID Q9LPT7 PRELIMINARY; PRT; 358 AA.
 AC Q9LPT7;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE FN18.15.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 RX NCBI_Taxid=3702;
 RA [1]
 RP SEQUENCE FROM N.A.
 RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
 RA Shih P., Altairi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lanz C., Li J., Liu A., Liu K., Liu S., Mukharly N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC FN18 from chromosome
 I.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; ACO17118; AAP25976.1;
 DR InterPro; IPR003441; NAM.
 DR Pfam; PF02365; NAM; 1.
 SQ SEQUENCE 358 AA; 41520 MW; 3C6F27668B0140F5 CRC64;
 Query Match 35.0%; Score 49; DB 10; Length 358;
 Best Local Similarity 46.7%; Pred. No. 2.9;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CRXNCRFQHLDDC 15
 Db 172 CRVFRKKNYKIDDC 186
 RESULT 11
 ID Q91902 PRELIMINARY; PRT; 721 AA.
 AC Q91902;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE X-delta-1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 OC Xenopodidae; Xenopus.
 RX NCBI_Taxid=8355;
 RA [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95319507; PubMed=7596411;
 RA Henrique D., Adam J., Myat A., Chltnis A., Lewis J., Ish-Horowitz D.;

RT "Expression of a Delta homologue in prospective neurons in the
 RT chick.";
 RL Nature 375:787-790(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95319503; PubMed=7596407;
 RA Chltnis A., Henrique D., Lewis J., Ish-Horowitz D., Kinter C.,
 RT "Primary neurogenesis in Xenopus embryos regulated by a homologue of
 RT the Drosophila neurogenic gene Delta.";
 RL Nature 375:761-766(1995).
 DR EMBL; L42229; AAC38017.1;
 DR HSSP; P00740; 1EDM.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001774; DSL.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF-2.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR001438; EGF_II.
 DR Pfam; PF01414; DSL; 1.
 DR Pfam; PF00008; EGF; 8.
 DR PRINTS; PR00010; EGFLOOD.
 DR SMART; SM00051; DSL; 1.
 DR SMART; SM00179; EGF_CA; 4.
 DR SMART; SM00001; EGF-like; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_3.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_8.
 DR PROSITE; PS01186; EGF_2; 8.
 DR PROSITE; PS01187; EGF_CA; 2.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
 SO SEQUENCE 721 AA; 79922 MW; 9EBDC85C439DD194 CRC64;
 Query Match 35.0%; Score 49; DB 13; Length 721;
 Best Local Similarity 38.1%; Pred. No. 5.4;
 Matches 8; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
 QY 6 QKCFQHLDDCCSXCNXNXC 26
 Db 440 RNCDDMLDDCTFPCONGGTC 460
 RESULT 12
 ID Q20204 PRELIMINARY; PRT; 1440 AA.
 AC Q20204;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE F40E10.4 protein.
 GN F40E10.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Rhabditinae; Caenorhabditis.
 RX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smye R.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RP [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Smye R.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z69792; CAA93668.2;
 DR EMBL; AL022270; CAA93668.2; JOINED.
 DR EMBL; AL022270; CAB63434.1;
 DR EMBL; Z69792; CAB63434.1; JOINED.
 DR HSSP; P00740; 1EDM.

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DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR001791; Lamlnln_G.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR003591; LRR_tyr.
DR Pfam: PF00008; EGF_7.
DR Pfam: PF00054; Lamlnln_G; 1.
DR Pfam: PF00560; LRR; 18.
DR Pfam: PF01453; LRRCT; 4.
DR Pfam: PF01452; LRRNT; 4.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00041; CT; 1.
DR SMART: SM00179; EGF_Ca; 2.
DR SMART: SM00001; EGF_like; 5.
DR SMART: SM00282; Lang; 1.
DR SMART: SM00370; LRR; 3.
DR SMART: SM00082; LRRCT; 4.
DR SMART: SM00013; LRRNT; 4.
DR SMART: SM00369; LRR_tyr; 7.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_7.
DR PROSITE: PS01186; EGF_2; 5.
DR PROSITE: PS01187; EGF_Ca; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SQ SEQUENCE 1440 AA; 161942 MW; 0B5D198645D3670 CRC64.

Query Match 35.0%; Score 49; DB 5; Length 1440;
Best Local Similarity 35.0%; Pred. No. 10;
Matches 7; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 8 CF0HLDCCSXXCNXNCV 27
DB 944 CEKNIDCVSKENGCKV 963

RESULT 13
061240 PRELIMINARY; PRT; 2352 AA.
AC 061240
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HmNotch protein.
GN HmNotch.
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxID=7729;
RX [1]
RP SEQUENCE FROM N.A.
RA Hori S., Satoh T., Matsumoto M., Makabe K.W., Nishida H.;
RT "Notch homologue from Halocynthia roretzi is preferentially expressed
RL in the central nervous system during ascidian embryogenesis."
DR EMBL: AB001327; BAA25571.1; -.
DR HSSP: P00740; IEDM.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR000800; Notch.
DR Pfam: PF00023; ank; 6.

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DR Pfam: PF00008; EGF; 32.
DR Pfam: PF00066; notch; 3.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR01452; NOTCH.
DR SMART: SM00248; ANK; 5.
DR SMART: SM00179; EGF_Ca; 17.
DR SMART: SM00001; EGF_like; 9.
DR SMART: SM00004; NL; 2.
DR PROSITE: PS50088; ANK_REPEAT; 5.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 18.
DR PROSITE: PS00022; EGF_1; UNKNOWN_28.
DR PROSITE: PS01186; EGF_2; 22.
DR PROSITE: PS01187; EGF_Ca; 18.
DR ANK repeat; Calcium-binding; EGF-like domain; Glycoprotein;
KW Hydroxylation; Repeat.
SQ SEQUENCE 2352 AA; 252623 MW; 13D1C056B0D08D CRC64;

Query Match 35.0%; Score 49; DB 5; Length 2352;
Best Local Similarity 35.0%; Pred. No. 16;
Matches 7; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 8 CF0HLDCCSXXCNXNCV 27
DB 452 CSONIDECASDPQMKATCI 471

RESULT 14
070244 PRELIMINARY; PRT; 3623 AA.
AC 070244
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Intrinsic factor-B12 receptor precursor.
GN CUBILIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RX [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98148073; PubMed-9478979;
RA Moestrup S.K., Koziyaki R., Kristiansen M., Kayser J.H.,
RA Rasmussen H.H., Brault D., Pontillon F., Goda F.O., Christensen E.I.,
RA Hammond T.G., Verroust P.J.;
RT "The intrinsic factor-vitamin B12 receptor and target of teratogenic
RT antibodies is a megalin-binding peripheral membrane protein with
RT homology to developmental proteins."
RL J. Biol. Chem. 273:5235-5242(1998).
CC -1- SIMILARITY: CONTAINS 26 CUB DOMAINS.
DR EMBL: AF022247; AAC71661.1; -.
DR HSSP: P00740; IEDM.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR Pfam: PF00431; CUB; 27.
DR Pfam: PF00008; EGF; 7.
DR SMART: SM00042; CUB; 26.
DR SMART: SM00179; EGF_Ca; 4.
DR SMART: SM00001; EGF_like; 4.
DR PROSITE: PS00010; ASX_HYDROXYL; 3.
DR PROSITE: PS01180; CUB; 27.
DR PROSITE: PS00022; EGF_1; UNKNOWN_4.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_Ca; 4.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;
KW Receptor; Repeat; signal.
FT SIGNAL 1
FT CHAIN 21 3623
SQ SEQUENCE 3623 AA; 398981 MW; 39FB92AC6545240 CRC64;

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Query Match 35.08; Score 49; DB 11; Length 3623;
 Best Local Similarity 31.88; Pred. No. 23;
 Matches 7; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

OY 6 OKCFQHLDDCCSXKXCNXXNCV 27
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 DB 427 ONCTENINDCSSNPCLNGCTCI 448

RESULT 15

O23456 PRELIMINARY; PRT; 1208 AA.
 AC O23456.
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE ZK287.4 protein.
 GN ZK287.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McMurray A.A.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL: Z70757; CA94800.1; -.
 DR HSSP; P31713; ISHP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR InterPro; IPR002899; WRI/EB.
 DR Pfam; PF00014; Kunitz_BPTI; 7.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 6.
 DR SMART; SM00131; KU; 7.
 DR SMART; SM00289; WRI; 3.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 7.
 DR Serine protease inhibitor.
 KW SEQUENCE 1208 AA; 133055 MW; F5BABF7D81BDE229 CRC64;

Query Match

Best Local Similarity 34.68; Score 48.5; DB 5; Length 1208;
 Matches 10; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

OY 5 NOKCFQHLDDCCSXKXCNXXNCV 26
 |||||
 DB 805 NONNFQSFDS-CSRACGATNVC 825

Search completed: January 14, 2003, 18:29:05
 Job time : 32 secs

Sequence Family Search of Proteins (/sqsf)

In the sequence family search, each amino acid in the query has to match either the exact amino acid or a family member equivalent, as shown in the Family Equivalence Table below. The Family Equivalence Table is applied only to each common amino acid in the sequence. Specific uncommon amino acids may be included in the sequence; however, family equivalents only exist for the common amino acids. An amino acid family is based on a conservative substitution of amino acids sharing a similar chemical property. Each common amino acid in the query is converted to its family class members in a search. A match occurs on a query sequence if each amino acid is exactly matched or any of its family members are encountered. For example, the Hydrophobic-Aromatic family consists of the common amino acids F, W, and Y. If the amino acid F is specified within a sequence exact family search, it will match on amino acids F, W, or Y.

FAMILY EQUIVALENCE TABLE

Family Class Name	Family Class Members
Neutral-Weakly Hydrophobic	Ala (A), Gly (G), Pro (P), Ser (S), Thr (T)
Hydrophilic-Acid Amine	Asn (N), Asp (D), Gln (Q), Glu (E)
Hydrophilic-Basic	Arg (R), His (H), Lys (K)
Hydrophobic	Ile (I), Met (M), Leu (L), Val (V)
Hydrophobic-Aromatic	Phe (F), Trp (W), Tyr (Y)
Crosslinking	Cys (C)

=> fil reg; d que 12
FILE 'REGISTRY' ENTERED AT 08:39:59 ON 15 JAN 2003
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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Property values tagged with IC are from the ZIC/VINITI data file
provided by InfoChem.

STRUCTURE FILE UPDATES: 14 JAN 2003 HIGHEST RN 479024-64-1
DICTIONARY FILE UPDATES: 14 JAN 2003 HIGHEST RN 479024-64-1

TSCA INFORMATION NOW CURRENT THROUGH MAY 20, 2002

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP
PROPERTIES for more information. See STNote 27, Searching Properties
in the CAS Registry File, for complete details:
<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

(L2 12 SEA FILE=REGISTRY ABB=ON CRI'HYP'NQKCFQHLDDCCS/SQSFP)

=> d rn cn sql kwic nte 12 1-12; fil capl; s 12

L2 ANSWER 1 OF 12 REGISTRY COPYRIGHT 2003 ACS

RN 332843-22-8) REGISTRY - Use registry # to match sequence to citation - CA reference #3

CN Peptide, (Cys-Arg-Ile-Xaa-Asn-Gln-Lys-Cys-Phe-Gln-His-Leu-Asp-Asp-Cys-Cys-
Ser-Xaa-Xaa-Cys-Asn-Xaa-Xaa-Asn-Xaa-Cys-Val) (9CI) (CA INDEX NAME)

SQL 27

SEQ 1 CRIXNQKCFQ HLDDCCSXXC NXXNXCXV

=====

HITS-AT: 1-17

NTE

type	location			description
uncommon	Hyp-4	-	-	
uncommon	Aaa-18	-	-	
uncommon	Aaa-19	-	-	
uncommon	Aaa-22	-	-	
uncommon	Aaa-23	-	-	
uncommon	Aaa-25	-	-	

L2 ANSWER 2 OF 12 REGISTRY COPYRIGHT 2003 ACS

RN 331640-80-3) REGISTRY - CA answer #3

CN L-Alanine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-
asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-
histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-
cysteinyl-L-seryl-L-arginyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-arginyl-L-
phenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic
(1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI) (CA
INDEX NAME)

SQL 27

SEQ 1 CRIXNQKCFQ HLDDCCSRKC NRFNKCA

HITS AT: 1-17

NTE

type	location	description
bridge	Cys-1 - Cys-16	disulfide bridge
bridge	Cys-8 - Cys-20	disulfide bridge
bridge	Cys-15 - Cys-26	disulfide bridge
uncommon	Hyp-4 -	-

L2 ANSWER 3 OF 12 REGISTRY COPYRIGHT 2003 ACS

RN 331640-76-7 REGISTRY CA reference # 3

CN L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-seryl-L-arginyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-arginyl-L-phenylalanyl-L-alanyl-L-lysyl-L-cysteinyl-, cyclic
(1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI) (CA
INDEX NAME)

SQL 27

SEQ 1 CRIXNQKCFQ HLDDCCSRKC NRFAKCV

HITS AT: 1-17

NTE

type	location	description
bridge	Cys-1 - Cys-16	disulfide bridge
bridge	Cys-8 - Cys-20	disulfide bridge
bridge	Cys-15 - Cys-26	disulfide bridge
uncommon	Hyp-4 -	-

L2 ANSWER 4 OF 12 REGISTRY COPYRIGHT 2003 ACS

RN 331640-75-6 REGISTRY CA reference # 3

CN L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-alanyl-L-arginyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-arginyl-L-phenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic
(1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI) (CA
INDEX NAME)

SQL 27

SEQ 1 CRIXNQKCFQ HLDDCCARKC NRFNKCVC

HITS AT: 1-17

NTE

type	location	description
bridge	Cys-1 - Cys-16	disulfide bridge
bridge	Cys-8 - Cys-20	disulfide bridge
bridge	Cys-15 - Cys-26	disulfide bridge
uncommon	Hyp-4 -	-

L2 ANSWER 5 OF 12 REGISTRY COPYRIGHT 2003 ACS

RN 331640-74-5 REGISTRY CA reference # 3

CN L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-

asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-seryl-L-arginyl-L-lysyl-L-cysteinyl-L-alanyl-L-arginyl-L-phenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic
(1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI) (CA
INDEX NAME)

SQL 27

SEQ 1 CRIXNQKCFQ HLDDCCSRKC ARFNKCV

=====

HITS AT: 1-17

NTE

type	location		description
bridge	Cys-1	- Cys-16	disulfide bridge
bridge	Cys-8	- Cys-20	disulfide bridge
bridge	Cys-15	- Cys-26	disulfide bridge
uncommon	Hyp-4	-	-

L2 ANSWER 6 OF 12 REGISTRY COPYRIGHT 2003 ACS

RN 331640-69-8 REGISTRY *CA reference #3*

CN L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-tyrosyl-L-glutaminyl-L-histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-seryl-L-arginyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-phenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic
(1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI) (CA
INDEX NAME)

SQL 27

SEQ 1 CRIXNQKCYQ HLDDCCSRKC NRFNKCV

=====

HITS AT: 1-17

NTE

type	location		description
bridge	Cys-1	- Cys-16	disulfide bridge
bridge	Cys-8	- Cys-20	disulfide bridge
bridge	Cys-15	- Cys-26	disulfide bridge
uncommon	Hyp-4	-	-

L2 ANSWER 7 OF 12 REGISTRY COPYRIGHT 2003 ACS

RN 331640-66-5 REGISTRY *CA reference #3*

CN L-Valine, L-cysteinyl-L-lysyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-seryl-L-arginyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-phenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic
(1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI) (CA
INDEX NAME)

SQL 27

SEQ 1 CKIXNQKCFQ HLDDCCSRKC NRFNKCV

=====

HITS AT: 1-17

NTE

type	location		description
------	----------	--	-------------

bridge	Cys-1	- Cys-16	disulfide bridge
bridge	Cys-8	- Cys-20	disulfide bridge
bridge	Cys-15	- Cys-26	disulfide bridge
uncommon	Hyp-4	-	-

L2 ANSWER 8 OF 12 REGISTRY COPYRIGHT 2003 ACS

RN 331640-65-4 REGISTRY CA reference # 3

CN L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-seryl-L-arginyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-arginyl-L-phenylalanyl-L-asparaginyl-L-alanyl-L-cysteinyl-, cyclic
(1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI) (CA
INDEX NAME)

SQL 27

SEQ 1 CRIXNQKCFQ HLDDCCSRKC NRFNACV

HITS AT: 1-17

NTE

type	location		description
bridge	Cys-1	- Cys-16	disulfide bridge
bridge	Cys-8	- Cys-20	disulfide bridge
bridge	Cys-15	- Cys-26	disulfide bridge
uncommon	Hyp-4	-	-

L2 ANSWER 9 OF 12 REGISTRY COPYRIGHT 2003 ACS

RN 331640-62-1 REGISTRY CA reference # 3

CN L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-seryl-L-arginyl-L-alanyl-L-cysteinyl-L-asparaginyl-L-arginyl-L-phenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic
(1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI) (CA
INDEX NAME)

SQL 27

SEQ 1 CRIXNQKCFQ HLDDCCSRAC NRFNKC

HITS AT: 1-17

NTE

type	location		description
bridge	Cys-1	- Cys-16	disulfide bridge
bridge	Cys-8	- Cys-20	disulfide bridge
bridge	Cys-15	- Cys-26	disulfide bridge
uncommon	Hyp-4	-	-

L2 ANSWER 10 OF 12 REGISTRY COPYRIGHT 2003 ACS

RN 331640-60-9 REGISTRY CA reference # 3

CN L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-seryl-L-arginyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-alanyl-L-phenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic
(1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI) (CA
INDEX NAME)

SQL 27

SEQ 1 CRIXNQKCFQ HLDDCCSRKC NAFNKCVC

=====

HITS AT: 1-17

NTE

type	location	description
bridge	Cys-1 - Cys-16	disulfide bridge
bridge	Cys-8 - Cys-20	disulfide bridge
bridge	Cys-15 - Cys-26	disulfide bridge
uncommon	Hyp-4 -	-

L2 ANSWER 11 OF 12 REGISTRY COPYRIGHT 2003 ACS

RN 331640-59-6 REGISTRY *CA reference # 3*

CN L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-seryl-L-alanyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-arginyl-L-phenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic
(1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI) (CA INDEX NAME)

SQL 27

SEQ 1 CRIXNQKCFQ HLDDCCSAKC NRFNKCVC

=====

HITS AT: 1-17

NTE

type	location	description
bridge	Cys-1 - Cys-16	disulfide bridge
bridge	Cys-8 - Cys-20	disulfide bridge
bridge	Cys-15 - Cys-26	disulfide bridge
uncommon	Hyp-4 -	-

L2 ANSWER 12 OF 12 REGISTRY COPYRIGHT 2003 ACS

RN 196605-79-57 REGISTRY *CA references 1-11*

CN .kappa.-Conotoxin P VIIA (9CI) (CA INDEX NAME)

OTHER NAMES:

CN L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-seryl-L-arginyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-arginyl-L-phenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic
(1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide)

SQL 27

SEQ 1 CRIXNQKCFQ HLDDCCSRKC NRFNKCVC

=====

HITS AT: 1-17

NTE

type	location	description
bridge	Cys-1 - Cys-16	disulfide bridge
bridge	Cys-8 - Cys-20	disulfide bridge
bridge	Cys-15 - Cys-26	disulfide bridge
uncommon	Hyp-4 -	-

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FILE LAST UPDATED: 14 Jan 2003 (20030114/ED)

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L3 11 L2] *Registry file answer set crossed into CAPLUS to get citations*
=> d ibib ab hitrn 1-11; fil hom

L3 ANSWER 1 OF 11 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:420792 CAPLUS
DOCUMENT NUMBER: 137:136264
TITLE: Inhibition of single Shaker K channels by
.kappa.-conotoxin-PVIIA
AUTHOR(S): Naranjo, David
CORPORATE SOURCE: Instituto de Fisiologia Celular, Universidad Nacional
Autonoma de Mexico, Circuito Exterior, Mexico, 04510,
Mex.
SOURCE: Biophysical Journal (2002), 82(6), 3003-3011
CODEN: BIOJAU; ISSN: 0006-3495
PUBLISHER: Biophysical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB .kappa.-Conotoxin-PVIIA (.kappa.-PVIIA) is a 27-residue basic (+4) peptide from the venom of the predator snail *Conus purpurascens*. A single .kappa.-PVIIA mol. interrupts ion conduction by binding to the external mouth of Shaker K channels. The blockade of Shaker by .kappa.-PVIIA was studied at the single channel level in membrane patches from *Xenopus* oocytes. The amplitudes of blocked and closed events were undistinguishable, suggesting that the toxin interrupts ion conduction completely. Between -20 and 40 mV .kappa.-PVIIA increased the latency to the first opening by one order of magnitude in a concn.-independent fashion. Because .kappa.-PVIIA has higher affinity for the closed channels at high enough concn. to block >90% of the resting channels, the disocn. rate could be estd. from the anal. of the first latency. At 0 mV, the disocn. rate was 20 s⁻¹ and had an effective valence of 0.64. The apparent closing rate increased linearly with [.kappa.-PVIIA] indicating an assocn. rate of 56 .mu.M⁻¹ s⁻¹. The toxin did not modify the fraction of null traces. This result suggests that the structural rearrangements in the external mouth contributing to the slow inactivation preserve the main geometrical features of the toxin-receptor interaction.

Use Registry # to match citation to sequence in Registry record

IT 196605-79-5, .kappa.-Conotoxin-PVIIA

RL: BSU (Biological study, unclassified); BIOL (Biological study)
(inhibition of single Shaker K channels by .kappa.-conotoxin-PVIIA)

REFERENCE COUNT: 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 2 OF 11 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:872474 CAPLUS

DOCUMENT NUMBER: 136:258891

TITLE: Molecular simulation of the interaction of
.kappa.-conotoxin-PVIIA with the Shaker potassium
channel pore

AUTHOR(S): Moran, Oscar

CORPORATE SOURCE: CNR, Istituto di Cibernetica e Biofisica, Genoa,
16149, Italy

SOURCE: European Biophysics Journal (2001), 30(7), 528-536
CODEN: EBJOE8; ISSN: 0175-7571

PUBLISHER: Springer-Verlag

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Mol. simulation techniques were applied to predict the interaction of the voltage-dependent Shaker potassium channel with the channel-blocking toxin .kappa.-conotoxin-PVIIA (PVIIA). A structural three-dimensional model of the extracellular vestibule of the potassium channel was constructed based on structural homologies with the bacterial potassium channel Kcsa, whose structure has been solved by x-ray crystallog. The docking of the PVIIA mol. was obtained by a geometric recognition algorithm, yielding 100 possible conformations. A series of residue-residue distance restraints, predicted from mutation-cycle expts., were used to select a small set of a plausible channel-toxin complex models among the resulting possible conformations. The four final conformations, with similar characteristics, can explain most of the single-point mutation expts. done with this system. The models of the Shaker-PVIIA interaction predict two clusters of amino acids, crit. for the binding of the toxin to the channel. The first cluster is the amino acids R2, I3, Q6 and K7 that form the plug of the toxin that interacts with the entrance to the selectivity filter of the channel. The second cluster of residues, R22, F23, N24 and K25, interacts with a channel region near to the external entrance of the pore vestibule. The consistency of the obtained models and the exptl. data indicate that the Shaker-PVIIA complex model is reasonable and can be used in further biol. studies such as the rational design of blocking agents of potassium channels and the mutagenesis of both toxins and potassium channels.

IT 196605-79-5, .kappa.-Conotoxin-PVIIA

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(complexes with potassium channel; mol. simulation of the interaction
of .kappa.-conotoxin-PVIIA with the Shaker potassium channel pore)

REFERENCE COUNT: 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 3 OF 11 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:228916 CAPLUS

DOCUMENT NUMBER: 134:275775

TITLE: .kappa.-Conotoxin PVIIA and analogs and derivatives
for activating ATP-sensitive potassium channels, and
therapeutic use

INVENTOR(S): Cornelli-Bell, Ann H.; Pemberton, Karen E.; Temple,
Davis L., Jr.; Layer, Richard T.; McCabe, R. Tyler;
Jones, Robert R.

PATENT ASSIGNEE(S): Cognetix, Inc., USA

SOURCE: PCT Int. Appl., 46 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001021648	A1	20010329	WO 2000-US25827	20000921
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1218407	A1	20020703	EP 2000-965219	20000921
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				
PRIORITY APPLN. INFO.:			US 1999-155135P	P 19990922
			US 2000-219438P	P 20000720
			WO 2000-US25827	W 20000921
OTHER SOURCE(S): MARPAT 134:275775				
AB	The invention relates to uses of .kappa.-conotoxin PVIIA, analogs and derivs. for activating ATP-sensitive potassium channels. The activation of ATP-sensitive potassium channels is useful for opening KATP channels which can be used to treat a wide range of disease and injury states, including cerebral and cardiac ischemia and asthma.			
IT	331640-59-6 331640-59-6D, derivs. 331640-60-9) 331640-60-9D, derivs. 331640-62-1 331640-62-1D) , derivs. 331640-65-4 331640-65-4D, derivs. 331640-66-5 331640-66-5D, derivs. 331640-69-8) 331640-69-8D, derivs. 331640-74-5 331640-74-5D) , derivs. 331640-75-6 331640-75-6D, derivs. 331640-76-7 331640-76-7D, derivs. 331640-80-3) 331640-80-3D, derivs. 332843-22-8)			
	RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)			
	(.kappa.-conotoxin PVIIA and analogs and derivs. for activating ATP-sensitive potassium channels, and therapeutic use)			
IT	196605-79-5, .kappa.-CONOTOXIN P VIIA 196605-79-5D, .kappa.-CONOTOXIN P VIIA, analogs and derivs.			
	RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)			
	(.kappa.-conotoxin PVIIA and analogs and derivs. for activating ATP-sensitive potassium channels, and therapeutic use)			
REFERENCE COUNT:	2	THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT		
L3	ANSWER 4 OF 11 CAPLUS COPYRIGHT 2003 ACS			
ACCESSION NUMBER:	2000:579029 CAPLUS			
DOCUMENT NUMBER:	133:292139			
TITLE:	Single amino acid substitutions in .kappa.-Conotoxin PVIIA disrupt interaction with the Shaker K ⁺ channel			
AUTHOR(S):	Jacobsen, Richard B.; Koch, E. Dietlind; Lange-Malecki, Bettina; Stocker, Martin; Verhey, Janko; Van Wagoner, Ryan M.; Vyazovkina, Alexandra; Olivera, Baldomero M.; Terlau, Heinrich			
CORPORATE SOURCE:	Departments of Biology and Medicinal Chemistry, University of Utah, Salt Lake City, UT, 84112, USA			

SOURCE: Journal of Biological Chemistry (2000), 275(32),
24639-24644
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular
Biology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB .kappa.-Conotoxin PVIIA (.kappa.-PVIIA), a 27-amino acid peptide with
three disulfide crosslinks, isolated from the venom of *Conus purpurascens*,
is the first conopeptide shown to inhibit the Shaker K⁺ channel.
Recently, two groups independently detd. the soln. structure for
.kappa.-PVIIA using NMR; although the structures reported were similar,
two mutually exclusive models for the interaction of the peptide with the
Shaker channel were proposed. The authors carried out a
structure/function anal. of .kappa.-PVIIA, with alanine substitutions for
all amino acids postulated to be key residues by both groups. The
authors' data are consistent with the crit. dyad model developed by Menez
and co-workers for polypeptide antagonists of K⁺ channels. In the case of
.kappa.-PVIIA, Lys7 and Phe9 are essential for activity as predicted by
Savarin et al. these workers also correctly predicted an important role
for Lys25. Thus, although .kappa.-conotoxin PVIIA has no obvious sequence
homol. to polypeptide toxins from other venomous animals that interact
with voltage-gated K⁺ channels, there may be convergent functional
features in diverse K⁺ channel polypeptide antagonists.
IT 196605-79-5) .kappa.-Conotoxin P VIIA
RL: ADV (Adverse effect, including toxicity); PRP (Properties); BIOL
(Biological study)
(single amino acid substitutions in .kappa.-Conotoxin PVIIA disrupt
interaction with the Shaker K⁺ channel)

REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 5 OF 11 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2000:191100 CAPLUS
DOCUMENT NUMBER: 132:237373
TITLE: Preparation of cyclized conotoxin peptides
INVENTOR(S): Craik, David James; Daly, Norelle Lee; Nielsen,
Katherine Justine
PATENT ASSIGNEE(S): University of Queensland, Australia
SOURCE: PCT Int. Appl., 43 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000015654	A1	20000323	WO 1999-AU769	19990914
W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
AU 9960705	A1	20000403	AU 1999-60705	19990914
AU 747006	B2	20020509		
EP 1129106	A1	20010905	EP 1999-947111	19990914
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			

PRIORITY APPLN. INFO.:

AU 1998-5895 A 19980914
WO 1999-AU769 W 19990914

AB Cyclized conotoxin peptides were prepd. for the therapeutic treatment of mammals. Thus, cyclo[CKGKGAKCSRLMYDCCTGSCRSGKCTRNLPG], a cyclic analog of MVIIA having the linking moiety TRNLPG, was prepd. by the solid-phase method.

IT **196605-79-5DP**, γ .kappa.-Conotoxin P VIIA, cyclic analogs
RL: SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(prepn. of cyclized conotoxin peptides)

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1999:477426 CAPLUS

DOCUMENT NUMBER: 131:253554

TITLE: A marine snail neurotoxin shares with scorpion toxins
a convergent mechanism of blockade on the pore of
voltage-gated K channels

AUTHOR(S): Garcia, Esperanza; Scanlon, Martin; Naranjo, David
CORPORATE SOURCE: Centro de Investigaciones Biomedicas, Universidad de
Colima, Colima, 28045, Mex.

SOURCE: Journal of General Physiology (1999), 114(1), 141-157
CODEN: JGPLAD; ISSN: 0022-1295

PUBLISHER: Rockefeller University Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB γ .kappa.-Conotoxin-PVIIA (γ .kappa.-PVIIA) belongs to a family of peptides derived from a hunting marine snail that targets to a wide variety of ion channels and receptors. γ .kappa.-PVIIA is a small, structurally constrained, 27-residue peptide that inhibits voltage-gated K channels. Three disulfide bonds shape a characteristic four-loop folding. The spatial localization of pos. charged residues in γ .kappa.-PVIIA exhibits strong structural mimicry to that of charybdotoxin, a scorpion toxin that occludes the pore of K channels. The authors studied the mechanism by which this peptide inhibits Shaker K channels expressed in *Xenopus* oocytes with the N-type inactivation removed. Chronically applied to whole oocytes or outside-out patches, γ .kappa.-PVIIA inhibition appears as a voltage-dependent relaxation in response to the depolarizing pulse used to activate the channels. At any applied voltage, the relaxation rate depended linearly on the toxin concn., indicating a bimol. stoichiometry. Time consts. and voltage dependence of the current relaxation produced by chronic applications agreed with that of rapid applications to open channels. Effective valence of the voltage dependence, $z.\delta$, is ≈ 0.55 and resides primarily in the rate of dissocn. from the channel, while the assocn. rate is voltage independent with a magnitude of $107\text{--}108\text{ M}^{-1}\text{s}^{-1}$, consistent with diffusion-limited binding. Compatible with a purely competitive interaction for a site in the external vestibule, tetraethylammonium, a well-known K-pore blocker, reduced γ .kappa.-PVIIA's assocn. rate only. Removal of internal K^+ reduced, but did not eliminate, the effective valence of the toxin dissocn. rate to a value < 0.3 . This trans-pore effect suggests that: (a) as in the α -KTx, a pos. charged side chain, possibly a Lys, interacts electrostatically with ions residing inside the Shaker pore, and (b) a part of the toxin occupies an externally accessible K^+ binding site, decreasing the degree of pore occupancy by permeant ions. The authors conclude that, although evolutionarily distant to scorpion toxins, γ .kappa.-PVIIA shares with them a remarkably similar mechanism of inhibition of K channels.

IT **196605-79-5**, γ .kappa.-Conotoxin-PVIIA

RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
(neurotoxin of marine snail shares with scorpion toxins a convergent mechanism of blockade on the pore of voltage-gated K (potassium)

channels)

REFERENCE COUNT: 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 7 OF 11 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1999:477425 CAPLUS

DOCUMENT NUMBER: 131:253553

TITLE: The block of Shaker K⁺ channels by .kappa.-conotoxin PVIIA is state dependent

AUTHOR(S): Terlau, Heinrich; Boccaccio, Anna; Olivera, Baldomero M.; Conti, Franco

CORPORATE SOURCE: Max-Planck-Institut fur Experimentelle Medizin, Gottingen, 37075, Germany

SOURCE: Journal of General Physiology (1999), 114(1), 125-140
CODEN: JGPLAD; ISSN: 0022-1295

PUBLISHER: Rockefeller University Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB .kappa.-Conotoxin PVIIA is the first conotoxin known to interact with voltage-gated potassium channels by inhibiting Shaker-mediated currents. The authors studied the mechanism of inhibition and concluded that PVIIA blocks the ion pore with a 1:1 stoichiometry and that binding to open or closed channels is very different. Open-channel properties are revealed by relaxations of partial block during step depolarizations, whereas double-pulse protocols characterize the slower reequilibration of closed-channel binding. In 2.5 mM-[K]⁺_o, the IC₅₀ rises from a tonic value of .apprx.50 to .apprx.200 nM during openings at 0 mV, and it increases e-fold for about every 40-mV increase in voltage. The change involves mainly the voltage dependence and a 20-fold increase at 0 mV of the rate of PVIIA disocn., but also a fivefold increase of the assocn. rate. PVIIA binding to Shaker .DELTA.6-46 channels lacking N-type inactivation or to wild phenotypes appears similar, but inactivation partially protects the latter from open-channel unblock. Raising [K]⁺_o to 115 mM has little effect on open-channel binding, but increases almost 10-fold the tonic IC₅₀ of PVIIA due to a decrease by the same factor of the toxin rate of assocn. to closed channels. In analogy with charybdotoxin block, the authors attribute the acceleration of PVIIA disocn. from open channels to the voltage-dependent occupancy by K⁺ ions of a site at the outer end of the conducting pore. The authors also argue that the occupancy of this site by external cations antagonizes on binding to closed channels, whereas the apparent competition disappears in open channels if the competing cation can move along the pore. It is concluded that PVIIA can also be a valuable tool for probing the state of ion permeation inside the pore.

IT (196605-79-5) .kappa.-Conotoxin PVIIA

RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
(shaker K⁺ (potassium) channels block by .kappa.-conotoxin PVIIA is state dependent)

REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 8 OF 11 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1998:276339 CAPLUS

DOCUMENT NUMBER: 129:37385

TITLE: Three-dimensional structure of .kappa.-conotoxin PVIIA, a novel potassium channel-blocking toxin from cone snails

AUTHOR(S): Savarin, Philippe; Guenneugues, Marc; Gilquin, Bernard; Lamthanh, Hung; Gasparini, Sylvanie; Zinn-Justin, Sophie; Menez, Andre

CORPORATE SOURCE: CE Saclay, Dep. Ing. Et. Proteines, CEA, Gif-sur-Yvette, 91191, Fr.

SOURCE: Biochemistry (1998), 37(16), 5407-5416

CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB .kappa.-Conotoxin PVIIA from the venom of *Conus purpurascens* is the first cone snail toxin that was described to block potassium channels. We synthesized chem. this toxin and showed that its disulfide bridge pattern is similar to those of .omega.- and .delta.-conotoxins. .kappa.-Conotoxin competes with radioactive .alpha.-dendrotoxin for binding to rat brain synaptosomes, confirming its capacity to bind to potassium channels; however, it behaves as a weak competitor. The three-dimensional structure of .kappa.-conotoxin PVIIA, as elucidated by NMR spectroscopy and mol. modeling, comprises two large parallel loops stabilized by a triple-stranded antiparallel .beta.-sheet and three disulfide bridges. The overall fold of .kappa.-conotoxin is similar to that of calcium channel-blocking .omega.-conotoxins but differs from those of potassium channel-blocking toxins from sea anemones, scorpions, and snakes. Local topogs. of .kappa.-conotoxin PVIIA that might account for its capacity to recognize Kvl-type potassium channels are discussed.

IT ~~196605=79-5P~~.kappa.-Conotoxin PVIIA
RL: PRP (Properties); SPN (Synthetic preparation); PREP (Preparation)
(three-dimensional structure of .kappa.-conotoxin PVIIA, novel potassium channel-blocking toxin from cone snails)

L3 ANSWER 9 OF 11 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1998:60152 CAPLUS
DOCUMENT NUMBER: 128:137369
TITLE: Solution structure and proposed binding mechanism of a novel potassium channel toxin .kappa.-conotoxin PVIIA
AUTHOR(S): Scanlonl, Martin J.; Naranjo, David; Thomas, Linda; Alewood, Paul F.; Lewis, Richard J.; Craik, David J.
CORPORATE SOURCE: Centre for Drug Design, University of Queensland, St. Lucia, 4072, Australia
SOURCE: Structure (London) (1997), 5(12), 1585-1597
CODEN: STRUE6; ISSN: 0969-2126
PUBLISHER: Current Biology Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The three-dimensional structure of PVIIA resembles the triple-stranded .beta. sheet/cystine-knot motif formed by a no. of toxic and inhibitory peptides. Subtle structural differences, predominantly in loops 2 and 4, are obsd. between PVIIA and other conotoxins with similar structural frameworks, however. Electrophysiol. binding data suggest that PVIIA blocks channel currents by binding in a voltage-sensitive manner to the external vestibule and occluding the pore. Comparison of the electrostatic surface of PVIIA with that of the well-characterized potassium channel blocker charybdotoxin suggests a likely binding orientation for PVIIA. Although the structure of PVIIA is considerably different to that of the .alpha.K scorpion toxins, it has a similar mechanism of channel blockade. On the basis of a comparison of the structures of PVIIA and charybdotoxin, we suggest that Lys19 of PVIIA is the residue which is responsible for phys. occluding the pore of the potassium channel.

IT ~~196605=79-5P~~.kappa.-Conotoxin PVIIA
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(soln. structure and potassium channel blocking activity of .kappa.-conotoxin PVIIA)

L3 ANSWER 10 OF 11 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1998:39008 CAPLUS
DOCUMENT NUMBER: 128:111749
TITLE: .kappa.-Conotoxin PVIIA is a peptide inhibiting the

AUTHOR(S): Shaker K⁺ channel
Shon, Ki-Joon; Stocker, Martin; Terlau, Heinrich;
Stuhmer, Walter; Jacobsen, Richard; Walker, Craig;
Grilley, Michelle; Watkins, Maren; Hillyard, David R.;
Gray, William R.; Olivera, Baldomero M.
CORPORATE SOURCE: Department of Physiology and Biophysics, Case Western
Reserve University, Cleveland, OH, 44106, USA
SOURCE: Journal of Biological Chemistry (1998), 273(1), 33-38
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular
Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB .kappa.-Conotoxin PVIIA (.kappa.-PVIIA), a 27-amino acid toxin from *Conus purpurascens* venom that inhibits the Shaker potassium channel, was chem. synthesized in a biol. active form. The disulfide connectivity of the peptide was detd. This is the first *Conus* peptide known to target K⁺ channels. Although the Shaker K⁺ channel is sensitive to .kappa.-PVIIA, the rat brain Kv1.1 subtype is resistant. Chimeras between Shaker and the Kv1.1 K⁺ channels were constructed and expressed in *Xenopus* oocytes. Only channels contg. the putative pore-forming region between the fifth and sixth transmembrane domains of Shaker retained toxin sensitivity, indicating that the toxin target site is in this region of the channel. Evidence is presented that .kappa.-PVIIA interacts with the external tetraethyl-ammonium binding site on the Shaker channel. Although both .kappa.-PVIIA and charybdotoxin inhibit the Shaker channel, they must interact differently. The F425G Shaker mutation increases charybdotoxin affinity by 3 orders of magnitude but abolishes .kappa.-PVIIA sensitivity. The precursor sequence of .kappa.-PVIIA was deduced from a cDNA clone, revealing a prepropeptide comprising 72 amino acids. The N-terminal region of the .kappa.-PVIIA prepropeptide exhibits striking homol. to the .omega.-, .mu.O-, and .delta.-conotoxins. Thus, at least four pharmacol. distinct superfamilies of *Conus* peptides belong to the same "O" superfamily, with the .omega.- and .kappa.-conotoxins forming one branch, and the .delta.- and .mu.O-conotoxins forming a second major branch.

IT ~~196605-79-5P~~ .kappa.-Conotoxin PVIIA
RL: PRP (Properties); PUR (Purification or recovery); PREP (Preparation)
(.kappa.-Conotoxin PVIIA inhibition of Shaker K⁺ channel)

L3 ANSWER 11 OF 11 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1997:640695 CAPLUS
DOCUMENT NUMBER: 127:274085
TITLE: Conotoxin peptide PVIIa
INVENTOR(S): Terlau, Heinrich; Shon, Ki-Joon; Grilley, Michelle M.;
Olivera, Baldomero M.
PATENT ASSIGNEE(S): University of Utah Research Foundation, USA
SOURCE: PCT Int. Appl., 29 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9734925	A1	19970925	WO 1997-US3483	19970314
W: AU, CA, JP				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 5672682	A	19970930	US 1996-619936	19960318
CA 2248710	AA	19970925	CA 1997-2248710	19970314
AU 9720690	A1	19971010	AU 1997-20690	19970314
AU 724408	B2	20000921		
EP 922055	A1	19990616	EP 1997-908897	19970314

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, FI

JP 2001500474 T2 20010116 JP 1997-533505 19970314
PRIORITY APPLN. INFO.: US 1996-619936 A 19960318
WO 1997-US3483 W 19970314

AB A new peptide, .kappa.-conotoxin PVIIA, is disclosed. This peptide is found naturally in the cone snail *Conus purpurascens* and has the amino acid sequence Cys-Arg-Ile-Xaa-Asn-Gln-Lys-Cys-Phe-Gln-His-Leu-Asp-Asp-Cys-Cys-Ser-Arg-Lys-Cys-Asn-Arg-Phe-Asn-Lys-Cys-Val where Xaa represents 4-trans-hydroxyproline, hydroxyproline or proline. This peptide together with a previously disclosed peptide, .delta.-conotoxin PVIA, act synergistically to rapidly immobilize fish which are injected with the two peptides. Injection of .kappa.-conotoxin PVIIA alone results in different symptoms with an injected fish becoming hyperactive and then contracting and suddenly extending all major fins. This fin-popping occurs repeatedly resulting in a series of jerky movements, but injection of only .kappa.-conotoxin PVIIA does not immobilize or kill the fish.

IT **196605-79-5P,** .kappa.-Conotoxin P VIIA

RL: ADV (Adverse effect, including toxicity); PRP (Properties); PUR
(Purification or recovery); BIOL (Biological study); PREP (Preparation)
(conotoxin peptide PVIIa)

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